

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: November 1, 2005, 18:03:08 ; Search time 7593 Seconds
(without alignments)
10748.990 Million cell updates/sec

Title: US-10-030-294-1

Perfect score: 5676

Sequence: 1 cagctgttcaggatgtctg.....tttataattgttcttcgt 5676

Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 27724519 seqs, 7189665201 residues

Total number of hits satisfying chosen parameters: 55449038

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Pending Patents_NA_New.*

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1: /cgn2_6/ptodata/1/pna/PCT_NEW_COMB.seq.*
2: /cgn2_6/ptodata/1/pna/PCT_NEW_COMB.seq2.*
3: /cgn2_6/ptodata/1/pna/US06_NEW_COMB.seq.*
4: /cgn2_6/ptodata/1/pna/US07_NEW_COMB.seq.*
5: /cgn2_6/ptodata/1/pna/US08_NEW_COMB.seq.*
6: /cgn2_6/ptodata/1/pna/US09_NEW_COMB.seq.*
7: /cgn2_6/ptodata/1/pna/US09_NEW_COMB.seq1.*
8: /cgn2_6/ptodata/1/pna/US09_NEW_COMB.seq2.*
9: /cgn2_6/ptodata/1/pna/US10_NEW_COMB.seq.*
10: /cgn2_6/ptodata/1/pna/US10_NEW_COMB.seq10.*
11: /cgn2_6/ptodata/1/pna/US10_NEW_COMB.seq11.*
12: /cgn2_6/ptodata/1/pna/US10_NEW_COMB.seq2.*
13: /cgn2_6/ptodata/1/pna/US10_NEW_COMB.seq3.*
14: /cgn2_6/ptodata/1/pna/US10_NEW_COMB.seq4.*
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24: /cgn2_6/ptodata/1/pna/US11_NEW_COMB.seq5.*
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26: /cgn2_6/ptodata/1/pna/US11_NEW_COMB.seq7.*
27: /cgn2_6/ptodata/1/pna/US11_NEW_COMB.seq8.*
28: /cgn2_6/ptodata/1/pna/US60_NEW_COMB.seq.*

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1987.4	35.0	255679	15	US-10-940-774A-17189, A
2	632.6	11.1	633	7	US-09-925-065A-552295, A
3	357.4	6.3	999	10	US-10-301-480C-842014, A
4	357.4	6.3	999	17	US-10-301-480C-344792, A
5	357.4	6.3	999	19	US-10-301-480B-344792, A

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c 6 196.2 3.5 65793 13 US-10-703-817-3
7 193.8 3.4 536 7 US-09-925-065A-552295
8 193.8 3.4 536 10 US-10-301-480C-906314
9 193.8 3.4 536 17 US-10-301-480A-906314
10 193.8 3.4 536 18 US-10-301-480A-530245
11 193.8 3.4 536 18 US-10-301-480-1143654
12 193.8 3.4 536 19 US-10-301-480B-906314
13 193.8 3.4 80503 15 US-10-990-328A-94591
14 192.2 3.4 536 7 US-09-925-065A-552294
15 192.2 3.4 536 10 US-10-301-480C-906313
16 192.2 3.4 536 17 US-10-301-480A-906313
17 192.2 3.4 536 18 US-10-301-480-530244
18 192.2 3.4 536 18 US-10-301-480-1143653
19 192.2 3.4 536 19 US-10-301-480B-906313
20 190.6 3.4 265038 15 US-10-940-774A-15779
21 190.6 3.4 300351 15 US-10-990-328A-96853
22 190.2 3.4 163565 15 US-10-950-328A-93556
23 188.8 3.3 874 10 US-10-301-480C-259257
24 188.8 3.3 874 17 US-10-301-480A-259257
25 188.8 3.3 874 19 US-10-301-480B-259257
26 187.6 3.3 739 10 US-10-301-480C-259258
27 187.6 3.3 739 17 US-10-301-480A-259258
28 187.6 3.3 739 19 US-10-301-480B-259258
29 187 3.3 997 10 US-10-301-480C-256336
30 187 3.3 997 17 US-10-301-480A-256336
31 187 3.3 997 19 US-10-301-480B-256336
32 186.8 3.3 991 10 US-10-301-480C-283512
33 186.8 3.3 991 17 US-10-301-480A-283512
34 186.8 3.3 991 19 US-10-301-480B-283512
35 186.8 3.3 992 10 US-10-301-480C-283513
36 186.8 3.3 992 17 US-10-301-480A-283513
37 186.8 3.3 992 19 US-10-301-480B-283513
38 186.6 3.3 652661 15 US-10-990-328A-97235
39 186.4 3.3 601 15 US-10-940-774A-142852
40 186 3.3 585 10 US-10-301-480C-597588
41 186 3.3 585 17 US-10-301-480A-597588
42 186 3.3 585 18 US-10-301-480-221519
43 186 3.3 585 18 US-10-301-480-834928
44 186 3.3 585 19 US-10-301-480B-597588
45 186 3.3 587 7 US-09-925-065A-123687

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ALIGNMENTS

RESULT 1

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US-10-940-774A-17189
; Sequence 17189, Application US/10940774A
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/10/940,774A
; CURRENT FILING DATE: 2004-09-15
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 17189
; LENGTH: 255679
; TYPE: DNA
; ORGANISM: Human
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (1) ..(255679)
; OTHER INFORMATION: n = A,T,C or G
US-10-940-774A-17189

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Sequence 906313,
Sequence 94591, A
Sequence 552294,
Sequence 906313,
Sequence 906313,
Sequence 530244,
Sequence 1143653,
Sequence 906313,
Sequence 15779, A
Sequence 96853, A
Sequence 93556, A
Sequence 259257,
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Sequence 97235, A
Sequence 142852,
Sequence 597588,
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Sequence 597588,
Sequence 221519,
Sequence 834928,
Sequence 597588,
Sequence 123687,

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Query Match		35.0%; Score 1987.4; DB 15; Length 255679;
Best Local Similarity		99.9%; Pred. No. 1.8e-254;
Matches 1999; Conservative		0; Mismatches 1; Indels 1; Gaps 1;
Qy	3676	TATCCCTGGAGTAAATTTAAATATTTAGAGAGTCTTCCCTCATTTCTTAGAGAGCTC 3735
Db	1	TATCCCTGGAGTAAATTTAAATATTTAGAGAGTCTTCCCTCATTTCTTAGAGAGCTC 60
Qy	3736	GAATTTGTAATATCAGAGCTAGAAGGAACACTAGGGCTGCGCACTCCAAAGTGTGGTCCA 3795
Db	61	GAAITGTAAATATCAGAGCTAGAAGGAACACTAGGGCTGCGCACTCCAAAGTGTGGTCCA 120
Qy	3796	AGGACGAGCAGCATCAAGTAACCTGGNAACGTGTAGAAATGCGAGTCTTAGGCTCAC 3855
Db	121	AGGACGAGCAGCATCAAGTAACCTGGNAACGTGTAGAAATGCGAGTCTTAGGCTCAC 180
Qy	3856	CCGAGACTCTGAACACAGAACTCTGCATTAAACAAGATTCTAGGTGCTCAGCGGCACAT 3915
Db	181	CCCAGACTCTGAACACAGAACTCTGCATTAAACAAGATTCTAGGTGCTCAGCGGCACAT 240
Qy	3916	TAAACTTTGAGAGCTCTGCAGTAAGAAATCTTCACTCCACCTTTTCATTATTAATGGAATC 3975
Db	241	TAAACTTTGAGAGCTCTGCAGTAAGAAATCTTCACTCCACCTTTTCATTATTAATGGAATC 300
Qy	3976	ACTTGGCTGTGTCACAGGAATTTGATTATTTTAAATTTTCAAGACCTTCTATTAGGTC 4035
Db	301	ACTT-GGCTGTGTCACAGGAATTTGATTATTTTAAATTTTCAAGACCTTCTATTAGGTC 359
Qy	4036	ATCTATATTTCTTAATACAGGAAGAAAGCCAACTCTTTAACTGCAATTTAAACAATCT 4095
Db	360	ATCTATATTTCTTAATACAGGAAGAAAGCCAACTCTTTAACTGCAATTTAAACAATCT 419
Qy	4096	ATAATTAATTAAGTAAAGCAATCTTCCCTTTAAAGTTTACATTTTGTGGAGCAAGCTGTT 4155
Db	420	ATAATTAATTAAGTAAAGCAATCTTCCCTTTAAAGTTTACATTTTGTGGAGCAAGCTGTT 479
Qy	4156	GATTTGGCTGGGCTCAGCGCGCTGTTGTGAATTTTCAAAATTCACAGATGTTAGCGG 4215
Db	480	GATTTGGCTGGGCTCAGCGCGCTGTTGTGAATTTTCAAAATTCACAGATGTTAGCGG 539
Qy	4216	CTCTCGGCTAAGTAAAGGAAGAGAACTCAAGTTTAAATAGCTTCTCCCTCCATCCT 4275
Db	540	CTCTCGGCTAAGTAAAGGAAGAGAACTCAAGTTTAAATAGCTTCTCCCTCCATCCT 599
Qy	4276	GGCTGAAGCAACAAATAAAATATTTTATGAACACATTTTGAAGTATTAATTAACAG 4335
Db	600	GGCTGAAGCAACAAATAAAATATTTTATGAACACATTTTGAAGTATTAATTAACAG 659
Qy	4336	GGAAATGTCAAAATTTCTGAAAGGCTTTAGATTGCTCACAAGTTTGACATCTACTGA 4395
Db	660	GGAAATGTCAAAATTTCTGAAAGGCTTTAGATTGCTCACAAGTTTGACATCTACTGA 719
Qy	4396	TGTCACCTATTATACAGGTGTCTGTGCACTAGGGGGTGAAGGAAGATGTGAATCTACC 4455
Db	720	TGTCACCTATTATACAGGTGTCTGTGCACTAGGGGGTGAAGGAAGATGTGAATCTACC 779
Qy	4456	ATGTTAGTGAACGTTTATACAGAGTGGTTTTTTTCCCTGTTGGAGTCTATACCTA 4515
Db	780	ATGTTAGTGAACGTTTATACAGAGTGGTTTTTTTCCCTGTTGGAGTCTATACCTA 839
Qy	4516	ACTGAGCTTCTGAATCATATTTCAATTTCCAAATCCAAACACAGGATAGTTTA 4575
Db	840	ACTGAGCTTCTGAATCATATTTCAATTTCCAAATCCAAACACAGGATAGTTTA 899
Qy	4576	CAGCCCATATTTCAGAAAGGAATAAATTTATTTGTGTAGACTTTTCTGATATTACACT 4635
Db	900	CAGCCCATATTTCAGAAAGGAATAAATTTATTTGTGTAGACTTTTCTGATATTACACT 959
Qy	4636	GATTTGGGAATATATGAACAAATTTTATGTTTTCTTTTGAAGTAGGTCAAGTCAAGGAA 4695
Db	960	GATTTGGGAATATATGAACAAATTTTATGTTTTCTTTTGAAGTAGGTCAAGTCAAGGAA 1019
Qy	4696	AACCAAAACACAAAACACTGTAAAGACATAAAGATAGGTGGCCGACTGAGAGATTA 4755

Db	1020	AACCAAAACAGCAAAACCTGTAAAGACATAAAGATAGAGTGGAGCCGACTGAGAGATTA 1079
Qy	4756	AAATAAACTAGAATATTTTATTAACAGGCAATTTGAAATAATTTGTGCACCTCAGAATA 4815
Db	1080	AAATAAACTAGAATATTTTATTAACAGGCAATTTGAAATAATTTGTGCACCTCAGAATA 1139
Qy	4816	TTCTACAATTAATATATTTTCCAAATTTTAAATATTTTAAAGAAATTTACTATATATG 4875
Db	1140	TTCTACAATTAATATATTTTCCAAATTTTAAATATTTTAAAGAAATTTACTATATATG 1199
Qy	4876	TAAGTACATGTGCATGTGTTTGGAGTAGGATTTAACTCAATAAAGGTTATTTCTTTT 4935
Db	1200	TAAGTACATGTGCATGTGTTTGGAGTAGGATTTAACTCAATAAAGGTTATTTCTTTT 1259
Qy	4936	ATTCCGGTCAGGCAAAAGCTTCTAAGGGGATGTGAAGGGATATCTCTTCTCTTAGCTGA 4995
Db	1260	ATTCCGGTCAGGCAAAAGCTTCTAAGGGGATGTGAAGGGATATCTCTTCTCTTAGCTGA 1319
Qy	4996	GAGGAAGCTGAGTCTTAAGTTAAATTAATCAAGGAATTTCCCTGCTTTTGTCTATTGA 5055
Db	1320	GAGGAAGCTGAGTCTTAAGTTAAATTAATCAAGGAATTTCCCTGCTTTTGTCTATTGA 1379
Qy	5056	GATTTGTCACACAACAGCGGTTGGCTGAAAGGGGAACTGAAAGGCGGGAGGAGGAA 5115
Db	1380	GATTTGTCACACAACAGCGGTTGGCTGAAAGGGGAACTGAAAGGCGGGAGGAGGAA 1439
Qy	5116	ATAGATGAAAAAACAACAAAACTTCCCTAAGAGCTCTACAAAAATTTTAGC 5175
Db	1440	ATAGATGAAAAAACAACAAAACTTCCCTAAGAGCTCTACAAAAATTTTAGC 1499
Qy	5176	CCCAGAAATAGTCACAGAAATCTCAATCAAAACAGTATCCAGATCAAGGAAGTGTTA 5235
Db	1500	CCCAGAAATAGTCACAGAAATCTCAATCAAAACAGTATCCAGATCAAGGAAGTGTTA 1559
Qy	5236	TGTAGCTGGAGCGGTGGACACTCATCAGCTCAGTTCAGTTTACAAAAGTCCAGGCTGCT 5295
Db	1560	TGTAGCTGGAGCGGTGGACACTCATCAGCTCAGTTCAGTTTACAAAAGTCCAGGCTGCT 1619
Qy	5296	GAAATTAACCTCTGATGCCATTCATGCCAGCATCCAATCAGCAGAGATCAGAAGTTCA 5355
Db	1620	GAAATTAACCTCTGATGCCATTCATGCCAGCATCCAATCAGCAGAGATCAGAAGTTCA 1679
Qy	5356	GAGATGCTCCAGCTCCAAATTTGCCAACACAGTGGCTACTATAGTCAAGGACTCT 5415
Db	1680	GAGATGCTCCAGCTCCAAATTTGCCAACACAGTGGCTACTATAGTCAAGGACTCT 1739
Qy	5416	GAAGCCGTGAGAGGGGGAAGAAACAACAGTAGAGAGGATGCCAGCTGGTAAAGAAATCGA 5475
Db	1740	GAAGCCGTGAGAGGGGGAAGAAACAACAGTAGAGAGGATGCCAGCTGGTAAAGAAATCGA 1799
Qy	5476	GTGTTTATGAAGTTTATGATCAATTTGATGAATCTCATTTGGCTTAAATCAAGAAAACGCTCG 5535
Db	1800	GTGTTTATGAAGTTTATGATCAATTTGATGAATCTCATTTGGCTTAAATCAAGAAAACGCTCG 1859
Qy	5536	CCTCTTTGCAATATGATGAAGGAGAGAGTGGCTTAACTTCTATGCTGATAGCATTT 5595
Db	1860	CCTCTTTGCAATATGATGAAGGAGAGAGTGGCTTAACTTCTATGCTGATAGCATTT 1919
Qy	5596	GACCCATTTGCTTTTAGCTCCCGCTTTATATCTATATATACAGGATTTTGTGTATA 5655
Db	1920	GACCCATTTGCTTTTAGCTCCCGCTTTATATCTATATATACAGGATTTTGTGTATA 1979
Qy	5656	TTTTATATAATTTGTTCTCCGT 5676
Db	1980	TTTTATATAATTTGTTCTCCGT 2000

RESULT 2
US-09-925-065A-842014
; Sequence 842014, Application US/09925065A
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.

; TITLE OF INVENTION: Identification and Mapping of Single
; FILE REFERENCE: 108827.135
; CURRENT APPLICATION NUMBER: US/09/925,065A
; PRIOR FILING DATE: 2001-08-08
; PRIOR APPLICATION NUMBER: US 60/243,096
; PRIOR FILING DATE: 2000-10-24
; PRIOR APPLICATION NUMBER: US 60/252,147
; PRIOR FILING DATE: 2000-11-20
; PRIOR APPLICATION NUMBER: US 60/250,092
; PRIOR FILING DATE: 2000-11-30
; PRIOR APPLICATION NUMBER: US 60/261,766
; PRIOR FILING DATE: 2001-01-16
; PRIOR APPLICATION NUMBER: US 60/289,846
; PRIOR FILING DATE: 2001-05-09
; NUMBER OF SEQ ID NOS: 957086
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 842014
; LENGTH: 633
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-925-065A-842014

Query Match 11.1%; Score 632.6; DB 7; Length 633;
Best Local Similarity 99.8%; Pred. No. 8.7e-75;
Matches 632; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
Qy 4064 AGCCAACTCTTTAACTGCAATTAACAAATCTATAATTAATAGTAAAGCAATCTCCCT 4123
Db 1 AGCCAACTCTTTAACTGCAATTAACAAATCTATAATTAATAGTAAAGCAATCTCCCT 60
Qy 4124 TTAAGTTTACATTTTGGAGCAAGCTGTTGATTTGGCTGGGGCTCAGCGCGCTGT 4183
Db 61 TTAAGTTTACATTTTGGAGCAAGCTGTTGATTTGGCTGGGGCTCAGCGCGCTGT 120
Qy 4184 TTGTGAATTTACAAATTCACAGATTTAGCGCTCTCGGCTAAGTAAGGAAGATG 4243
Db 121 TTGTGAATTTACAAATTCACAGATTTAGCGCTCTCGGCTAAGTAAGGAAGATG 180
Qy 4244 TCAAGTTTAAATAGCTTCTCCCTCCATCTGCTGAAGCAACAAATAAATATTTTAA 4303
Db 181 TCAAGTTTAAATAGCTTCTCCCTCCATCTGCTGAAGCAACAAATAAATATTTTAA 240
Qy 4304 TGAACAACATTTTCAGTTAGATTTTACTTACAGGAAATGTCAAAATTTCTCGAAAGGCT 4363
Db 241 TGAACAACATTTTCAGTTAGATTTTACTTACAGGAAATGTCAAAATTTCTCGAAAGGCT 300
Qy 4364 TTAGATTTGTCTCAAACTTTGACATCTACTGATGTCACTTATTTACAGGTGTCTCTGTG 4423
Db 301 TTAGATTTGTCTCAAACTTTGACATCTACTGATGTCACTTATTTACAGGTGTCTCTGTG 360
Qy 4424 ACTAGGGGGTGAAGGAAGATGTGAACCTCACCATGTTAGTGACCGTTAGATACACAGAT 4483
Db 361 ACTAGGGGGTGAAGGAAGATGTGAACCTCACCATGTTAGTGACCGTTAGATACACAGAT 420
Qy 4484 GGTFTTTTTTCCCTCTGTGGAGTCTATCTCTAACTAGCTTCTGAATCATATTTCAATCA 4543
Db 421 GGTFTTTTTTCCCTCTGTGGAGTCTATCTCTAACTAGCTTCTGAATCATATTTCAATCA 480
Qy 4544 ATTTCAAATCCAAACCAAGGATAGTTTACAGCCCATATTCAGAAAGGAATAAAT 4603
Db 481 ATTTCAAATCCAAACCAAGGATAGTTTACAGCCCATATTCAGAAAGGAATAAAT 540
Qy 4604 ATTTTGTGTGAGACTTTTCTGATATTACACTGATTTGGGAATATATGAACAATTTTATG 4663
Db 541 ATTTTGTGTGAGACTTTTCTGATATTACACTGATTTGGGAATATATGAACAATTTTATG 600
Qy 4664 GTTTCCTTTTGAAGTAGTCAAGTCAAGCAAA 4696
Db 601 GTTTCCTTTTGAAGTAGTCAAGTCAAGCAAA 633

RESULT 3

US-10-301-480C-344792
; Sequence 344792, Application US/10301480C
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single
; FILE REFERENCE: 108827-137
; CURRENT APPLICATION NUMBER: US/10/301,480C
; PRIOR FILING DATE: 2002-11-21
; PRIOR APPLICATION NUMBER: US 10/215,598
; PRIOR FILING DATE: 2002-08-09
; PRIOR APPLICATION NUMBER: US 60/311,695
; PRIOR FILING DATE: 2001-08-10
; NUMBER OF SEQ ID NOS: 989478
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 344792
; LENGTH: 999
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-301-480C-344792

Query Match 6.3%; Score 357.4; DB 10; Length 999;
Best Local Similarity 99.7%; Pred. No. 2.2e-38;
Matches 358; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
Qy 1 CAGCTGTTCAGGGATGTCTGAAAAGAGCCACCCACCATTTGCTTCTGGACACTGGGTGT 60
Db 641 CAGCTGTTCAGGGATGTCTGAAAAGAGAGCCACCCACCATTTGCTTCTGGACACTGGGTGT 700
Qy 61 GACTTTGGAGGGTATCAGGTTTGTCTGTTAAAGAACTGCCAACTTCTCTGCCCAAT 120
Db 701 GACTTTGGAGGGTATCAGGTTTGTCTGTTAAAGAACTGCCAACTTCTCTGCCCAAT 760
Qy 121 TGGCTCTGTTCCTTCGATGCCCTCTTCTTGGGACACTCCCTTAAGGCATCTTCTTG 180
Db 761 TGGCTCTGTTCCTTCGATGCCCTCTTCTTGGGACACTCCCTTAAGGCATCTTCTTG 820
Qy 181 ACATTAACCTTAACATATAAATGTTTATTTGATGAATTTTCAAGTACCTGAAGAGATGAG 240
Db 821 ACATTAACCTTAACATATAAATGTTTATTTGATGAATTTTCAAGTACCTGAAGAGATGAG 880
Qy 241 GTCAAAATCAGAAAGACACATGCTAAGTTGCAATGCACCTTGTCTTTTCAATTAATA 300
Db 881 GTCAAAATCAGAAAGACACATGCTAAGTTGCAATGCACCTTGTCTTTTCAATTAATA 940
Qy 301 AGTCATTGCAATACATTCAGTTTACTTAAAGTTCTAGGCCAGCTTTTACTCTTAATCA 359
Db 941 AGTCATTGCAATACATTCAGTTTACTTAAAGTTCTAGGCCAGCTTTTACTCTTAATCA 999

RESULT 4
US-10-301-480A-344792
; Sequence 344792, Application US/10301480A
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single
; FILE REFERENCE: 108827-137
; CURRENT APPLICATION NUMBER: US/10/301,480A
; PRIOR FILING DATE: 2002-11-21
; PRIOR APPLICATION NUMBER: US 10/215,598
; PRIOR FILING DATE: 2002-08-09
; PRIOR APPLICATION NUMBER: US 60/311,695
; PRIOR FILING DATE: 2001-08-10
; NUMBER OF SEQ ID NOS: 989478
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 344792
; LENGTH: 999
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-301-480A-344792

Query Match 6.3%; Score 357.4; DB 17; Length 999;

Best Local Similarity 99.7%; Pred. No. 2.2e-38;
Matches 358; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 CAGCTGTTCAAGGATGTCGAAAGAGAGCCACCCACATTTGCTTCTGGACACTGGGTGT 60
Db |||||
641 CAGCTGTTCAAGGATGTCGAAAGAGAGCCACCCACATTTGCTTCTGGACACTGGGTGT 700
Qy 61 GACTTTGGAGGGTATCAGGTTTGTCTGTTAAAGAAACTGCCAACCTTCTTCTGCCCAAT 120
Db |||||
701 GACTTTGGAGGGTATCAGGTTTGTCTGTTAAAGAAACTGCCAACCTTCTTCTGCCCAAT 760
Qy 121 TGGCCTCTGTTCCCTTGCATGCCCTCTTCTTCTGGGACACTCCCTTAAGGCATCTTCTTG 180
Db |||||
761 TGGCCTCTGTTCCCTTGCATGCCCTCTTCTTCTGGGACACTCCCTTAAGGCATCTTCTTG 820
Qy 181 ACATTAACTTAACATATAAATGTTTATTGATGAATTTTCAGTGACCTGAAGAGATGGAG 240
Db |||||
821 ACATTAACTTAACATATAAATGTTTATTGATGAATTTTCAGTGACCTGAAGAGATGGAG 880
Qy 241 GTCAAAATCAGAAGACACATGGCTAAGGTTTGCAATGCATCTGCTTTTTCATTGAATTA 300
Db |||||
881 GTCAAAATCAGAAGACACATGGCTAAGGTTTGCAATGCATCTGCTTTTTCATTGAATTA 940
Qy 301 AGTCATTCGAATACCATTCAGTTTACTTAAGTTCTAGGCCAGCTTTTACTCCTTAATCGA 359
Db |||||
941 AGTCATTCGAATACCATTCAGTTTACTTAAGTTCTAGGCCAGCTTTTACTCCTTAATCGA 999

RESULT 5

US-10-301-480B-344792
; Sequence 344792, Application US/10301480B
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single
; FILE REFERENCE: 108927-137
; CURRENT APPLICATION NUMBER: US/10/301.480B
; PRIOR FILING DATE: 2002-11-21
; PRIOR FILING DATE: 2002-08-09
; PRIOR FILING DATE: 2002-08-09
; PRIOR FILING DATE: 2001-08-10
; NUMBER OF SEQ ID NOS: 989478
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 344792
; LENGTH: 999
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-301-480B-344792

Query Match 6.3%; Score 357.4; DB 19; Length 999;
Best Local Similarity 99.7%; Pred. No. 2.2e-38;
Matches 358; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 CAGCTGTTCAAGGATGTCGAAAGAGAGCCACCCACATTTGCTTCTGGACACTGGGTGT 60
Db 641 CAGCTGTTCAAGGATGTCGAAAGAGAGCCACCCACATTTGCTTCTGGACACTGGGTGT 700
Qy 61 GACTTTGGAGGGTATCAGGTTTGTCTGTTAAAGAAACTGCCAACCTTCTTCTGCCCAAT 120
Db 701 GACTTTGGAGGGTATCAGGTTTGTCTGTTAAAGAAACTGCCAACCTTCTTCTGCCCAAT 760
Qy 121 TGGCCTCTGTTCCCTTGCATGCCCTCTTCTTCTGGGACACTCCCTTAAGGCATCTTCTTG 180
Db 761 TGGCCTCTGTTCCCTTGCATGCCCTCTTCTTCTGGGACACTCCCTTAAGGCATCTTCTTG 820
Qy 181 ACATTAACTTAACATATAAATGTTTATTGATGAATTTTCAGTGACCTGAAGAGATGGAG 240
Db 821 ACATTAACTTAACATATAAATGTTTATTGATGAATTTTCAGTGACCTGAAGAGATGGAG 880
Qy 241 GTCAAAATCAGAAGACACATGGCTAAGGTTTGCAATGCATCTGCTTTTTCATTGAATTA 300
Db 881 GTCAAAATCAGAAGACACATGGCTAAGGTTTGCAATGCATCTGCTTTTTCATTGAATTA 940

Qy 301 AGTCATTCGAATACCATTCAGTTTACTTAAGTTCTAGGCCAGCTTTTACTCCTTAATCGA 359
Db 941 AGTCATTCGAATACCATTCAGTTTACTTAAGTTCTAGGCCAGCTTTTACTCCTTAATCGA 999

RESULT 6

US-10-703-817-3/c
; Sequence 3, Application US/10703817
; GENERAL INFORMATION:
; APPLICANT: ROTH, RICHARD B.
; APPLICANT: NELSON, MATTHEW ROBERTS
; APPLICANT: KAMMERER, STEFAN M.
; APPLICANT: BRAUN, ANDREAS
; TITLE OF INVENTION: METHODS FOR IDENTIFYING RISK OF MELANOMA AND TREATMENTS
; FILE REFERENCE: SEQ-4061-UT
; CURRENT APPLICATION NUMBER: US/10/703.817
; CURRENT FILING DATE: 2003-11-06
; PRIOR APPLICATION NUMBER: 60/489,703
; PRIOR FILING DATE: 2003-07-23
; PRIOR APPLICATION NUMBER: 60/424,475
; PRIOR FILING DATE: 2002-11-06
; NUMBER OF SEQ ID NOS: 255
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 3
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-703-817-3

Query Match 3.5%; Score 196.2; DB 13; Length 65793;
Best Local Similarity 70.0%; Pred. No. 2.7e-17;
Matches 278; Conservative 0; Mismatches 118; Indels 1; Gaps 1;

Qy 3262 CTTTTAAATTTTTTAAAAAATAGATGAGTGTGGTGCCTCATGCTGTAAATCCCAACACT 3321
Db 18059 CTATAAAGTTTTTTTACAGGGAAGCCAGGTGCGGTGCTCACACCTGTAAATCCAGCACT 18000
Qy 3322 TTGGGAAGCCGGTTCGGAGGATAGCTTTAGTCCAGCAGTTTGGACAGCTCAGGGCAAC 3381
Db 17999 TTGGGAAGCTGAGCAGGTGGAATGCTTGAGCTCAGGAGTTTGAGACCAGCCTGGGCAAC 17940
Qy 3382 ACAGCAAGACCCATATCTTAAAAAACAACAAAAAATACCTGGGTATGTTGTG 3441
Db 17939 ATGGCAAAAAACCCATCTCTACATAAAATACAGAAAAAATTAGCTGCGAGTTGTTGGTG 17880
Qy 3442 CTCACCTGTAGTCCAAGCTACACAGGAAGCTGAGGCAAGAGGATCACTTTGAGCCCCAGGAG 3501
Db 17879 CACACCTGTGCTCTGCTTACTCAGGAGTCTGAGATGGGAGATTGCTTGAGCCCCAGAG 17820
Qy 3502 GTTGAGGCTCAGTGATCCATGAACGCGCTGCTACACT-CAGTCTGGGTGACAGTGCAG 3560
Db 17819 ATTGAGGCTCAGTGAGCCAAAGATCATGCCACTGTACTCCAGCCTGGGCAACAGAGCAAG 17760
Qy 3561 AAGCTGTCTCAAAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAA 3620
Db 17759 ACTCCATCTCAAAAAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAA 17700
Qy 3621 ATTTTAAAAACACAAACACTAGAGATGTTTGGCAAT 3657
Db 17699 TATAATATATACACACACATATATATATATATATATATATATATATATATATATAT 17663

RESULT 7

US-09-925-065A-552295
; Sequence 552295, Application US/09925065A
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single
; FILE REFERENCE: 108827.135
; CURRENT APPLICATION NUMBER: US/09/925.065A

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; CURRENT FILING DATE: 2001-08-08
; PRIOR APPLICATION NUMBER: US 60/243,096
; PRIOR FILING DATE: 2000-10-24
; PRIOR APPLICATION NUMBER: US 60/252,147
; PRIOR FILING DATE: 2000-11-20
; PRIOR APPLICATION NUMBER: US 60/250,092
; PRIOR FILING DATE: 2000-11-30
; PRIOR APPLICATION NUMBER: US 60/261,766
; PRIOR FILING DATE: 2001-01-16
; PRIOR APPLICATION NUMBER: US 60/289,846
; PRIOR FILING DATE: 2001-05-09
; NUMBER OF SEQ ID NOS: 957086
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 552295
; LENGTH: 536
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-925-065A-552295

Query Match      3.4%; Score 193.8; DB 7; Length 536;
Best Local Similarity 70.9%; Pred. No. 1.1e-16;
Matches 270; Conservative 1; Mismatches 108; Indels 2; Gaps 1;

QY 3212 ATCATGACATACGTTTAAATGATATTATTTAAATAGCTTTAGGCTATAAACCTTTTAAATT 3271
Db 1 ATCTGTACAAAACATCTGATTTTCAAAATCTTTAGGTAGTAAAGTTAAATCTA 60

QY 3272 TTTTAAAAAATAGATGAGTGTGGCTCATGCCCTGTAATCCCAACACTTTTGGGAAGCC 3331
Db 61 AAGGTCAAAGATTGCTGGGTATGTTAGCTACGCCCTGTAATTTCAAACACTTTAGGAGGCC 120

QY 3332 GGGTCGGGAGGATGAGTGTGAGTCCAGCAGTGTGAGCCAGTCAAGGCAACACAGCAAGAC 3391
Db 121 GAGGCGGGCGTATCGCTTGAGCCAGGGGTTTGAGACCAAGTAGTGGGCAACCAAGGCAAAAC 180

QY 3392 CCCATATCTAAAAAACAACAAAACAAAATTAATCTCGGTATGGTGTGCTCACCTGTA 3451
Db 181 CCCATCTTACAAAATAAAAATACA--ATAATGAGCTGGGCATGTTGGCAGCACCTGTG 238

QY 3452 GTCCAAAGCTACACAGGAAGCTGAGGCGAGAGGATCACTTTGAGCCAGGAGTTGAGGCTG 3511
Db 239 GTCCCAAGCTACTTTGGGAGGCTGAGGCGAGGAGTGCCTTGAGCCCAAGGAGTTGGGCTG 298

QY 3512 CAGTGATCCATGAACCGCTGCTTACACTCAGTCTGGGTGACAGTGCAGAAAGCTGTCTCA 3571
Db 299 CAGTGAGCTGTGACTGTACTTACTGCACTCCACCTAGTGCAGAGTAAGACCCCTGTCTCA 358

QY 3572 AAAATAATAAATAAATAAATAA 3592
Db 359 AAAATAAACAATAAATAAATAA 379

RESULT 9
US-10-301-480A-906314
; Sequence 906314, Application US/10301480A
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single
; Nucleotide Polymorphisms in the Human Genome
; FILE REFERENCE: 108827-137
; CURRENT APPLICATION NUMBER: US/10/301,480A
; PRIOR FILING DATE: 2002-11-21
; PRIOR APPLICATION NUMBER: US 10/215,598
; PRIOR FILING DATE: 2002-08-09
; PRIOR APPLICATION NUMBER: US 60/311,695
; PRIOR FILING DATE: 2001-08-10
; NUMBER OF SEQ ID NOS: 989478
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 906314
; LENGTH: 536
; TYPE: DNA
; ORGANISM: Homo sapien
US-10-301-480A-906314

Query Match      3.4%; Score 193.8; DB 17; Length 536;
Best Local Similarity 70.9%; Pred. No. 1.1e-16;
Matches 270; Conservative 1; Mismatches 108; Indels 2; Gaps 1;

QY 3212 ATCATGACATACGTTTAAATGATATTATTTAAATAGCTTTAGGCTATAAACCTTTTAAATT 3271
Db 1 ATCTGTACAAAACATCTGATTTTCAAAATCTTTAGGTAGTAAAGTTAAATCTA 60

QY 3272 TTTTAAAAAATAGATGAGTGTGGCTCATGCCCTGTAATCCCAACACTTTTGGGAAGCC 3331
Db 61 AAGGTCAAAGATTGCTGGGTATGTTAGCTACGCCCTGTAATTTCAAACACTTTAGGAGGCC 120

QY 3332 GGGTCGGGAGGATGAGTGTGAGTCCAGCAGTGTGAGCCAGTCAAGGCAACACAGCAAGAC 3391
Db 121 GAGGCGGGCGTATCGCTTGAGCCAGGGGTTTGAGACCAAGTAGTGGGCAACCAAGGCAAAAC 180

QY 3392 CCCATATCTAAAAAACAACAAAACAAAATTAATCTCGGTATGGTGTGCTCACCTGTA 3451
Db 181 CCCATCTTACAAAATAAAAATACA--ATAATGAGCTGGGCATGTTGGCAGCACCTGTG 238

QY 3452 GTCCAAAGCTACACAGGAAGCTGAGGCGAGAGGATCACTTTGAGCCAGGAGTTGAGGCTG 3511
Db 239 GTCCCAAGCTACTTTGGGAGGCTGAGGCGAGGAGTGCCTTGAGCCCAAGGAGTTGGGCTG 298

QY 3512 CAGTGATCCATGAACCGCTGCTTACACTCAGTCTGGGTGACAGTGCAGAAAGCTGTCTCA 3571
Db 299 CAGTGAGCTGTGACTGTACTTACTGCACTCCACCTAGTGCAGAGTAAGACCCCTGTCTCA 358

QY 3572 AAAATAATAAATAAATAAATAA 3592
Db 359 AAAATAAACAATAAATAAATAA 379

RESULT 8
US-10-301-480C-906314
; Sequence 906314, Application US/10301480C
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single
; Nucleotide Polymorphisms in the Human Genome
; FILE REFERENCE: 108827-137
; CURRENT APPLICATION NUMBER: US/10/301,480C
; PRIOR FILING DATE: 2002-11-21
; PRIOR APPLICATION NUMBER: US 10/215,598
; PRIOR FILING DATE: 2002-08-09
; PRIOR APPLICATION NUMBER: US 60/311,695
; PRIOR FILING DATE: 2001-08-10
; NUMBER OF SEQ ID NOS: 989478
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 906314
; LENGTH: 536
; TYPE: DNA
; ORGANISM: Homo sapien
US-10-301-480C-906314
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RESULT 11
US-10-301-480-1143654

US-10-301-480B-906314

Query Match 3.4%; Score 193.8; DB 19; Length 536;
Best Local Similarity 70.9%; Pred. No. 1.1e-16;
Matches 270; Conservative 1; Mismatches 108; Indels 2; Gaps 1;

QY 3212 ATCATGACATACGTTTAAATGATATTTAAATAGCTTAGGCTATAAACCTTTTAAATT 3271
DB 1 ATCTGTACAAAACATCTGATTTTCAAAATCTTTTAGGTAGTAAAGTTTAAATCTTA 60

QY 3272 TTTTAAAAAATAGATAGCTGTGGCTCATGCTGTAATCCCAACACTTTGGGAAGCC 3331
DB 61 AAGGTCAAAGATTGCTGGGTATGGTAGCTACGCTGTAAATCCCAACACTTAGGAGCC 120

QY 3332 GGGTCGGGAGGATAGCTTGAGTCCAGCAGTTTGAGACCAAGTCCAGGCAACAGCAAGAC 3391
DB 121 GAGGCGGGGTATCGCTTGAGCCAGGAGTTTGAGACCAAGTCCAGGCAACAGGCAAAAC 180

QY 3392 CCCATATCTAAAAAACAACAAAACAAAATTAATCTGGGTATGGTGTCTCACTGTA 3451
DB 181 CCCATCTTACAAAATAAAAATACAA--ATAATGAGCTGGGCATGGTGGCAGCACCTGTG 238

QY 3452 GTCCAAAGCTTACACGAAGCTCAGGCAGAAAGATCACTTTGAGCCAGGAGTTGAGGCTG 3511
DB 239 GTCCAGCTACTTGGGAGGCTGAGCAGGAGATGCTTTGAGCCAGGAGTTGGGGCTG 298

QY 3512 CAGTGATCCATGAACGCGCTGTACACTCAGTCTGGGTGACAGTGCAAGAAGCTGTCTCA 3571
DB 299 CAGTGAGCTGTACTGTACTGTCACTCCACTCAGTGTGACAGTAATGAGCCCTGTCTCA 358

QY 3572 AAAATAAATAAATAAAAA 3592
DB 359 AAAATAAATAAATAAAAA 379

RESULT 13

US-10-990-328A-94591/C
; Sequence 94591, Application US/10990328A
; GENERAL INFORMATION:
; APPLICANT: CARGILL, Michele
; TITLE OF INVENTION: POLYMORPHISMS IN NUCLEIC ACID MOLECULES
; TITLE OF INVENTION: ENCODING HUMAN ENZYME PROTEINS, METHODS OF DETECTION AND
; TITLE OF INVENTION: USES THEREOF
; FILE REFERENCE: CL001495
; CURRENT APPLICATION NUMBER: US/10/990,328A
; CURRENT FILING DATE: 2004-11-17
; NUMBER OF SEQ ID NOS: 558924
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 94591
; LENGTH: 80503
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)...(80503)
; OTHER INFORMATION: n = A,T,C or G
US-10-990-328A-94591

Query Match 3.4%; Score 193.8; DB 15; Length 80503;
Best Local Similarity 66.5%; Pred. No. 5.5e-17;
Matches 276; Conservative 1; Mismatches 138; Indels 0; Gaps 0;

QY 3233 ATATTATTAAATAGCTTAGGCTATAAACCTTTTAAATTTTAAAAAATAGATGAGTG 3292
DB 27708 AAAAAATTTAAATTTAGTAGAATAATATATTTTCAAAATGACAAAGTTAGGCCACACA 27649

QY 3293 TGGTGGCTCATGCTGTAAATCCCAACACTTTGGGAAGCCGGGTGCGGAGGATAGCTTGAG 3352
DB 27648 TGGTGGCTCACACCTGTAACTCAGCACTTTTGAAGGCTGAGGCGGAGGAGCTGCTTGAG 27589

QY 3353 TCCAGCAGTTTGAACCAAGTCCAGGCAACAGCAAGACCCCATATCTTAAAAAACAACAAA 3412
DB 27588 CCCAGGAGTTTGAACCAAGCTCCGCGCAACATAGCAAGACCCCTCTCTATAAATAACAAAC 27529

QY 3413 CAAAAAATAATTTACCTGGGTATGGTTGTCTCACTGTAGTCCAAAGCTACACAGGAAGCT 3472
DB 27528 GACAAATAATTTAGCAGGCGGTGGTGGTGCATGCTATGGTCCAGCTACTCAGGAGGCT 27469

QY 3473 GAGGCAAGAAGATCACTTTAGCCCAAGGAGTTGAGGCTCAGTGATCCATGAACGCGCTG 3532
DB 27468 GAGGCAAGGAGTATGCTGAGCTCAGGAGTCAAGGCTCAATAGCCATGATGACATCA 27409

QY 3533 CTACACTCAGTCTGGGTGACAGTCAAGAGCTGTCTCAAAATATAAATAAATAAATAA 3592
DB 27408 TTGCACTGAGCTGTGACAGCAAGACACTGTCTCCAAAAAATAAATAAATAAATAA 27349

QY 3593 TAACTTTTAAAAAACAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAA 3647
DB 27348 AAGGTTAAACCGCACATCATATTTGTTAGAGCAAAATATCATCTGAAAAAT 27294

RESULT 14

US-09-925-065A-552294
; Sequence 552294, Application US/09925065A
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single
; TITLE OF INVENTION: Nucleotide Polymorphisms in the Human Genome
; FILE REFERENCE: 108827.135
; CURRENT APPLICATION NUMBER: US/09/925,065A
; CURRENT FILING DATE: 2001-08-08
; PRIOR APPLICATION NUMBER: US 60/243,096
; PRIOR FILING DATE: 2000-10-24
; PRIOR APPLICATION NUMBER: US 60/252,147
; PRIOR FILING DATE: 2000-11-20
; PRIOR APPLICATION NUMBER: US 60/250,092
; PRIOR FILING DATE: 2000-11-30
; PRIOR APPLICATION NUMBER: US 60/261,766
; PRIOR FILING DATE: 2001-01-16
; PRIOR APPLICATION NUMBER: US 60/289,846
; PRIOR FILING DATE: 2001-05-09
; NUMBER OF SEQ ID NOS: 957086
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 552294
; LENGTH: 536
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-925-065A-552294

Query Match 3.4%; Score 192.2; DB 7; Length 536;
Best Local Similarity 70.6%; Pred. No. 1.8e-16;
Matches 269; Conservative 1; Mismatches 109; Indels 2; Gaps 1;

QY 3212 ATCATGACATACGTTTAAATCATATATTATTAATACGTTAGGCTATAAACCTTTTAAATT 3271
DB 1 ATCTGTACAAAACATCTGATTTTCAAAATCTTTTAGGTAGTAAAGTTTAAATCTTA 60

QY 3272 TTTTAAAAAATAGATGAGTGTGGTCTCATGCTGTAATCCCAACACTTTTGGGAAGCC 3331
DB 61 AAGGTCAAAGATTGCTGGGTATGGTGTAGCTCAGCCTGTAATTTCCAAACACTCTAGGAGCC 120

QY 3332 GGGTCGGGAGGATAGCTTTAGTCCAGCAGTTTGAAGCAGTCCAGGCAACAGCAAGAC 3391
DB 121 GAGGCGGGCTATCGCTTGAGCCAGGAGTTTGAAGCAGTCCAGGCAACAGGCAAAAC 180

QY 3392 CCCATATCTAAAAAACAACAAAACAAAATTAATCTGGGTATGGTGTCTGCTCACTGTA 3451
DB 181 CCCATCTTACAAAATAAAAATACAA--ATAATGAGCTGGGCATGGTGGCAGCACCTGTG 238

QY 3452 GTCCAAAGCTACACAGGAAGCTGAGGCAGAAAGATCACTTTGAGCCAGGAGTTGAGGCTG 3511
DB 239 GTCCAGCTACTTGGGAGGCTGAGGCAAGGATGGCTTGAGCCAGGATGTTGGGGCTG 298

QY 3512 CAGTGATCCATGAACGCGCTGTCTCACTCAGTCTGGGTGACAGTGCAAGAAGCTGTCTCA 3571
DB 299 CAGTGAGCTGTGACTGTACTGTCACTCCACTCAGTCCCACTAGGTGACAGAAATAGACCCCTGTCTCA 358

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OM nucleic - nucleic search, using sw model

Run on: November 1, 2005, 14:41:22 ; Search time 847 Seconds
(without alignments)
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Perfect score: 5676
Sequence: 1 cagctgttcaggatgctg.....tttataattgttctccgt 5676

Scoring table: IDENTITY NUC
Gapop 10.0 , Gapext 1.0

Searched: 1202784 seqs, 818138359 residues

Total number of hits satisfying chosen parameters: 2405568

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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5: /cgn2_6/ptodata/1/ina/PCTUS_COMB.seq.*

6: /cgn2_6/ptodata/1/ina/backfiles1.seq.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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1	1987.4	35.0	255679	4	US-09-949-016-17189, A
2	190.6	3.4	265038	4	US-09-949-016-15779, A
3	187.6	3.3	8133	3	US-09-659-791A-10
c 4	186.4	3.3	601	4	US-09-949-016-142852
5	186	3.3	17348	4	US-09-949-016-17403
c 6	185.6	3.3	601	4	US-09-949-016-201827
c 7	185.4	3.3	37292	4	US-09-949-016-15382
8	184.8	3.3	172677	4	US-09-949-016-13444
9	184.6	3.3	33272	4	US-09-949-016-16949
10	184.4	3.2	601	4	US-09-949-016-58699
11	184	3.2	601	4	US-09-949-016-132156
12	183.4	3.2	601	4	US-09-949-016-119415
c 13	182.8	3.2	36228	4	US-09-949-016-12256
c 14	182.8	3.2	36228	4	US-09-949-016-15468
c 15	182.6	3.2	134140	4	US-09-949-016-12672
c 16	182.6	3.2	134241	4	US-09-949-016-12424
c 17	182.6	3.2	134242	4	US-09-949-016-15813
c 18	182.6	3.2	134242	4	US-09-949-016-15814
c 19	182.6	3.2	134242	4	US-09-949-016-15815
c 20	182.4	3.2	601	4	US-09-949-016-132157
21	182.2	3.2	36651	3	US-09-738-894A-3
22	182.2	3.2	36651	4	US-09-964-469-3
c 23	182.2	3.2	51403	4	US-09-949-016-15057
c 24	181.8	3.2	4732	4	US-09-949-016-14962
25	181	3.2	601	4	US-09-949-016-127367
26	181	3.2	69924	4	US-09-949-016-15367
27	180.8	3.2	21920	4	US-09-949-016-15609

C	28	180.2	3.2	86273	4	US-09-949-016-15273	Sequence 15273, A
	29	180.2	3.2	87205	4	US-09-949-016-13430	Sequence 13430, A
	30	180	3.2	78720	4	US-09-949-016-12710	Sequence 12710, A
	31	180	3.2	78720	4	US-09-949-016-17283	Sequence 17283, A
	32	179.6	3.2	103377	4	US-09-949-016-14089	Sequence 14089, A
	33	179.6	3.2	119032	4	US-09-949-016-12160	Sequence 12160, A
	34	179.6	3.2	119032	4	US-09-949-016-17268	Sequence 17268, A
	35	179.6	3.2	163181	4	US-09-949-016-13730	Sequence 13730, A
	36	179.4	3.2	601	4	US-09-949-016-58698	Sequence 58698, A
C	37	179.2	3.2	77851	4	US-09-949-016-12508	Sequence 12508, A
C	38	179.2	3.2	77867	4	US-09-949-016-13211	Sequence 13211, A
C	39	179.2	3.2	77867	4	US-09-949-016-13212	Sequence 13212, A
C	40	179.2	3.2	77940	4	US-09-949-016-12509	Sequence 12509, A
	41	179	3.2	65848	4	US-09-949-016-13285	Sequence 13285, A
C	42	178.8	3.2	152132	4	US-09-949-016-13845	Sequence 13845, A
C	43	178.8	3.2	152145	4	US-09-949-016-12371	Sequence 12371, A
C	44	178.6	3.1	186734	4	US-09-949-016-14870	Sequence 14870, A
C	45	178.6	3.1	193689	4	US-09-949-016-12350	Sequence 12350, A

ALIGNMENTS

RESULT 1

US-09-949-016-17189

; Sequence 17189, Application US/09949016

; Patent No. 6812339

; GENERAL INFORMATION:

; APPLICANT: VENTER, J. Craig et al.

; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF

; FILE REFERENCE: CLO01307

; CURRENT APPLICATION NUMBER: US/09/949,016

; CURRENT FILING DATE: 2000-04-14

; PRIOR APPLICATION NUMBER: 60/241,755

; PRIOR FILING DATE: 2000-10-20

; PRIOR APPLICATION NUMBER: 60/237,768

; PRIOR FILING DATE: 2000-10-03

; PRIOR APPLICATION NUMBER: 60/231,498

; PRIOR FILING DATE: 2000-09-08

; NUMBER OF SEQ ID NOS: 207012

; SOFTWARE: FastSeq for Windows Version 4.0

; SEQ ID NO 17189

; LENGTH: 255679

; TYPE: DNA

; ORGANISM: Human

; FEATURE:

; NAME/KEY: misc feature

; LOCATION: (1)...(255679)

; OTHER INFORMATION: n = A,T,C or G

US-09-949-016-17189

Query Match	35.0%	Score	1987.4;	DB	4;	Length	255679;
Best Local Similarity	99.9%	Pred. No.	0;				
Matches	1999;	Conservative	0;	Mismatches	1;	Indels	1;
						Gaps	1;
Qy	3676	TATCCCTGGAAGTAAATTTTAAAGAGAGTTCCTTCCTCATTTCTAGAGAGCTC	3735				
Db	1	TATCCCTGGAAGTAAATTTTAAAGAGTTCCTTCCTCATTTCTAGAGAGCTC	60				
Qy	3736	GAATTGTAATATATCAGAGCTAGAGAACTAGGCTGCCACTCCAAAGTGTGTCCA	3795				
Db	61	GAATTGTAATATATCAGAGCTAGAGAACTAGGCTGCCACTCCAAAGTGTGTGTCCA	120				
Qy	3796	AGACACAGCAGCATCAAGTAACCTGGGACGCTGTAGAAATGAGAGTCTTAGGCCTCAC	3855				
Db	121	AGACACAGCAGCATCAAGTAACCTGGGACGCTGTAGAAATGAGAGTCTTAGGCCTCAC	180				
Qy	3856	CCAGACCTACTGAACACAGAACTGCAATTAACAAAGATTTCTAGGTGCTCACCAGGCACAT	3915				
Db	181	CCAGACCTACTGAACACAGAACTGCAATTAACAAAGATTTCTAGGTGCTCACCAGGCACAT	240				
Qy	3916	TAAACTTGAAGAGCTCTGCACCTAGAAATCTTCACTCCACCTTTTATTATAATGGAAATC	3975				

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Db 241 TAAACCTTGAGAGCTCTGACCTAGAAATCTTCACTCCACCTTTCAATTAATATGAATC 300
Qy 3976 ACTTGGGCTGTGTGCACAGAAATATGATTAATTTTAAATTTTCAGAACTTCTATTTAGGTC 4035
Db 301 ACTT-GGCTGTGTGCACAGAAATATGATTAATTTTAAATTTTCAGAACTTCTATTTAGGTC 359
Qy 4036 ATCTATATTTGCTTAAATAGCAGGGAAGAAAGCCAAACTCTTTAACTGCAATTAACAATCT 4095
Db 360 ATCTATATTTGCTTAAATAGCAGGGAAGAAAGCCAAACTCTTTAACTGCAATTAACAATCT 419
Qy 4096 ATAATTAATTAAGTAAAGCAATCTTCCCTTTAAGTTTTCACATTTTGGAGCAAGCTGTTT 4155
Db 420 ATAATTAATTAAGTAAAGCAATCTTCCCTTTAAGTTTTCACATTTTGGAGCAAGCTGTTT 479
Qy 4156 GATTTGGCTGGGCTCAGGCGGCTGTGTTGTGAATTTTCAATTTACAGATGTTAGCCG 4215
Db 480 GATTTGGCTGGGCTCAGGCGGCTGTGTTGTGAATTTTCAATTTACAGATGTTAGCCG 539
Qy 4216 CTCTCGGCTTAAGTAAAGGAAGAGATGTCAAGTTTAAATAGCTTCTCCCTTCCATCCT 4275
Db 540 CTCTCGGCTTAAGTAAAGGAAGAGATGTCAAGTTTAAATAGCTTCTCCCTTCCATCCT 599
Qy 4276 GGCTGAAGCAACAAATAAATAATTTTATGAACAATTTTGAATTTAGTTTACTTACAG 4335
Db 600 GGCTGAAGCAACAAATAAATAATTTTATGAACAATTTTGAATTTAGTTTACTTACAG 659
Qy 4336 GGAATGTCAAAATTTCTGTAAGGGCTTTAGATTTGTCACAACTTTGACATCTACTGA 4395
Db 660 GGAATGTCAAAATTTCTGTAAGGGCTTTAGATTTGTCACAACTTTGACATCTACTGA 719
Qy 4396 TGTCACTATTTACAGGTGTCTGTGACTAGGGGTGAAGGAGATGTGAACCTCACC 4455
Db 720 TGTCACTATTTACAGGTGTCTGTGACTAGGGGTGAAGGAGATGTGAACCTCACC 779
Qy 4456 ATGTTAGTGAACGTTAGATACACAGAGTGGTTTTTTTCCCTGTTGGAGTCTATCCTA 4515
Db 780 ATGTTAGTGAACGTTAGATACACAGAGTGGTTTTTTTCCCTGTTGGAGTCTATCCTA 839
Qy 4516 ACTGAGCTTCTGAATCATATTTCAATTTCAAAATTCACAAACAGGAGTAAGTTTA 4575
Db 840 ACTGAGCTTCTGAATCATATTTCAATTTCAAAATTCACAAACAGGAGTAAGTTTA 899
Qy 4576 CAGCCCATATTCAGAAAGGAAATAAATTAATTTGTGTGTAGACTTTCTCATATTAACACT 4635
Db 900 CAGCCCATATTCAGAAAGGAAATAAATTAATTTGTGTGTAGACTTTCTCATATTAACACT 959
Qy 4636 GATTTGGGAATATATGAACAAATTTTATGGTTTCTTTTCGAAGTAGGTCAAGTCAAAAGCAA 4695
Db 960 GATTTGGGAATATATGAACAAATTTTATGGTTTCTTTTCGAAGTAGGTCAAGTCAAAAGCAA 1019
Qy 4696 AACCAAAACAGCAAAACCTGTAAGACATAAAGATAGAGTGGCGGACTGAGATTA 4755
Db 1020 AACCAAAACAGCAAAACCTGTAAGACATAAAGATAGAGTGGCGGACTGAGATTA 1079
Qy 4756 AAATAAATAGATATTTTATTAACAGGCAATTTGAAATAATTTGTGCACTTCAGAAATA 4815
Db 1080 AAATAAATAGATATTTTATTAACAGGCAATTTGAAATAATTTGTGCACTTCAGAAATA 1139
Qy 4816 TTCTACAATAATATATTTTCCAAATTTTAAATATCTTTTAAAGAAATTAATCTATATATG 4875
Db 1140 TTCTACAATAATATATTTTCCAAATTTTAAATATCTTTTAAAGAAATTAATCTATATATG 1199
Qy 4876 TAAGTACATGTGATGTTTGGAGTAGGATTTTAACTCAATAAAGGTTATTTTCTTTT 4935
Db 1200 TAAGTACATGTGATGTTTGGAGTAGGATTTTAACTCAATAAAGGTTATTTTCTTTT 1259
Qy 4936 ATTTCGGCTCAGGCAAAAGCTTCTAAGGGGATGTGAAGGGATATCTTCTTCTTAGCTGA 4995
Db 1260 ATTTCGGCTCAGGCAAAAGCTTCTAAGGGGATGTGAAGGGATATCTTCTTCTTAGCTGA 1319
Qy 4996 GAGGAAGAGTGAGTCTTAAGTTAAATATAATCAAGGAATTTCCGTGCTTTGCTATTTGA 5055
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Db 1320 GAGGAAGAGTGAGTCTTAAGTTAAATATAATCAAGGAATTTCCCTGCTTTTGTCTATTGA 1379
Qy 5056 GATTTGTGACCAACAAGGCGGTTGGCTGAAAGGGAACCTGAAGGGCGGGAGGGAGGGA 5115
Db 1380 GATTTGTGACCAACAAGGCGGTTGGCTGAAAGGGAACCTGAAGGGCGGGAGGGAGGGA 1439
Qy 5116 ATAGATGAAAAAACAACAACAACAACAACAACAACAACAACAACAACAACAACAACAACA 5175
Db 1440 ATAGATGAAAAAACAACAACAACAACAACAACAACAACAACAACAACAACAACAACAACA 1499
Qy 5176 CCAGAAATAGTCACAGAAATCTTCAAAATCAAAACCAAGTATCCAGATACAAAGGAAGTTA 5235
Db 1500 CCAGAAATAGTCACAGAAATCTTCAAAATCAAAACCAAGTATCCAGATACAAAGGAAGTTA 1559
Qy 5236 TGTAGCTGAGCAGGCTGACACTCATCAGCTCAGTTTCAAAAGTTCACAAAGTCCAGGCTGCT 5295
Db 1560 TGTAGCTGAGCAGGCTGACACTCATCAGCTCAGTTTCAAAAGTTCACAAAGTCCAGGCTGCT 1619
Qy 5296 GAAATTTAAACTCTGATGCCATTCATGCCAGCATCCAATCAGCAGAGATCAGAAGTTCA 5355
Db 1620 GAAATTTAAACTCTGATGCCATTCATGCCAGCATCCAATCAGCAGAGATCAGAAGTTCA 1679
Qy 5356 GAGATGCCCTCCAGCTCAAAATGCCAAACAAGTGTGGCTACTATACGTCAGAGACTCT 5415
Db 1680 GAGATGCCCTCCAGCTCAAAATGCCAAACAAGTGTGGCTACTATACGTCAGAGACTCT 1739
Qy 5416 GAAGCGCTCAGAGAGGGGAAGCAACAAGTAGAGAGGATGCCAGCTGTAAGATCGA 5475
Db 1740 GAAGCGCTCAGAGAGGGGAAGCAACAAGTAGAGAGGATGCCAGCTGTAAGATCGA 1799
Qy 5476 GTGTTTATGAAAGTTTGTAGTCAATTTGATGAATCTCATTTGGCTAAATCAAGAAACGCTCCG 5535
Db 1800 GTGTTTATGAAAGTTTGTAGTCAATTTGATGAATCTCATTTGGCTAAATCAAGAAACGCTCCG 1859
Qy 5536 CTTCTTTGCAATAATGATGAAGGAGAGAGTGCCTAAATCTTCTATGCTGATAGCATTT 5595
Db 1860 CTTCTTTGCAATAATGATGAAGGAGAGAGTGCCTAAATCTTCTATGCTGATAGCATTT 1919
Qy 5596 GACCTTATTTGCTTTAGCTCCCGCTTTATATCTATATATACACAGGATTTTGTGTATA 5655
Db 1920 GACCTTATTTGCTTTAGCTCCCGCTTTATATCTATATATACACAGGATTTTGTGTATA 1979
Qy 5656 TTTTATATAATTTGTTCTCCGT 5676
Db 1980 TTTTATATAATTTGTTCTCCGT 2000
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RESULT 2

```
US-09-949-016-15779
; Sequence 15779, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; PRIOR FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 15779
; LENGTH: 265038
; TYPE: DNA
; ORGANISM: Human
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)...(265038)
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OTHER INFORMATION: n = A,T,C or G
US-09-949-016-15779

Query Match 3.4%; Score 190.6; DB 4; Length 265038;
Best Local Similarity 74.8%; Pred. No. 2.9e-33;
Matches 252; Conservative 0; Mismatches 84; Indels 1; Gaps 1;

QY 3257 TAAACCTTTTAAATTTTAAAAAATAGATGTGGTGGCTCATGCTGTAATCCCA 3316
DB 31960 TAAATTTTATAAGATCAAAACCATGGCAGCGGTGTATGCTCAGCCCTGTCATCCCA 32019
QY 3317 ACATTTTGGAGCCGGTGGGAGGATAGTTCAGTCCAGCAGTTTGACACCAAGTCCAGG 3376
DB 32020 GCACTTTGGAGGCCAAGGAGGAGGATGCTTGAGCCCGAGGATTCGAGACCAAGCTGG 32079
QY 3377 GCAACACAGCAAGACCCCATATCTTAAAAAACAACAAAAAATACCTGGGTATGG 3436
DB 32080 GCAACATAGTGAGACCTGTCTATAAAAAATCAAGCAAAATAGCCGGTGTGA 32139
QY 3437 TTGTGCTACCTGTAGTCCAAAGCTACACAGAAAGCTGAGGAGGATCACTTGAGCCC 3496
DB 32140 TGGCGCATGCTGTAGTCCAGCTACTCAAGAGGCTAAGCGGGAGGATGCTTGAGCCT 32199
QY 3497 AGAGGTTGAGGCTGCAATCATCAAGCCGCTGTACACT-CAGTCTGGGTGACAGT 3555
DB 32200 GGGAAATTGAGGCTGCAATCATCAAGCCGCTGTACACT-CAGTCTGGGTGACAGT 32259
QY 3556 GCAAGAGCTGTCTCAAAAAATAAATAAATAAATAA 3592
DB 32260 GCAAGACCTGTCTCAAAAAAATAAATAAATAAATAA 32296

RESULT 3
US-09-659-791A-10
; Sequence 10, Application US/09659791A
; Patent No. 6383808
; GENERAL INFORMATION:
; APPLICANT: Brett P. Monia
; TITLE OF INVENTION: ANTISENSE MODULATION OF CLUSTERIN EXPRESSION
; FILE REFERENCE: RTS-0156
; CURRENT APPLICATION NUMBER: US/09/659,791A
; CURRENT FILING DATE: 2000-09-11
; NUMBER OF SEQ ID NOS: 90
; SEQ ID NO 10
; LENGTH: 8133
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-659-791A-10

Query Match 3.3%; Score 187.6; DB 3; Length 8133;
Best Local Similarity 74.6%; Pred. No. 3.3e-33;
Matches 249; Conservative 0; Mismatches 84; Indels 1; Gaps 1;

QY 3264 TTTAAATTTTAAAAAATAGATGTGGTGGCTCATGCTGTAATCCCAACACTTT 3323
DB 1057 TTTAAAGAGGAAAAAATCAGCTGGGATGGTGGCTCATGCTGTGATGCCACACTTT 1116
QY 3324 GGGAGCCGGTGGGAGGATAGTTCAGTCCAGCAGTTTGAGACCAAGTCCAGGCAAC 3383
DB 1117 GAGAGCCAAAGCGGGAGGATCATTTGAGCCAGGAGTTTGAGACCAAGCTGGCCAA 1176
QY 3384 AGCAAGACCCCATATCTTAAAAAACAACAAAAAATACCTGGGTATGGTTGTGCT 3443
DB 1177 AGTGAGACCTGTCTTACAAAAATAAATAAATTTAGCCGGTGTGGTGTGA 1236
QY 3444 CACTGTAGTCCAAAGCTACACAGAAAGCTGAGGAGGATCACTTGAGCCCAAGGAT 3503
DB 1237 CACTGTAGTCTCAGCTACTCGGAGGCTGAGGCAAGAGTCACTTGAGCCTGGAAGTT 1296
QY 3504 TGAGGCTGCAAGTATCATCAAGCCGCTGTACACT-CAGTCTGGGTGACAGTGCAGAA 3562
DB 1297 GGAGGCTGCAAGTATGATTCACCAATTCAGCCCTGGGCAACAGAGTGTAGAC 1356

QY 3563 GCTGTCTCAAAAAATAAATAAATAAATAAATAAATAC 3596
DB 1357 CCTGTCTCTAAATTTAAAAAATAAATAAATAAATAAATAC 1390

RESULT 4
US-09-949-016-142852/c
; Sequence 142852, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 142852
; LENGTH: 601
; TYPE: DNA
; ORGANISM: Human
US-09-949-016-142852

Query Match 3.3%; Score 186.4; DB 4; Length 601;
Best Local Similarity 78.0%; Pred. No. 2.1e-33;
Matches 237; Conservative 0; Mismatches 66; Indels 1; Gaps 1;

QY 3290 GTGTGGTCTCATGCTGTATCCCAACACTTTGGGAAGCCGGTGGGAGGATAGCTT 3349
DB 596 GCGTGTATGCTCAGCGCTGTATCCCAAGCAGCTTTGGGAGCCCAAGGAGGATGCTT 537
QY 3350 GAGTCAGCAGTGTGAGACCAAGTCAGGCAACAGCAAGCAAGCCCATATCTAAAAAACA 3409
DB 536 GAGCCAGGAGTTCGAGACCAAGCTGGGCAACATAGTGAGACCTGTCTCTATAAAAAA 477
QY 3410 AAAAACAACAAATACCTGGGTATGTTGTGTCTACCTGTAGTCCAGTACACAGAA 3469
DB 476 AAATCAAGCAAAATAGCCGGTGTGATGCGCATGCTGTAGTCCAGCTACTCAAGAG 417
QY 3470 GCTGAGGCAAGGATCACTTGAGCCCAAGGAGTTGAGGCTGAGTCCAGTATCCATGAACGG 3529
DB 416 GCTAAGCGGGAGGATGCTTGAGCCCTGGGAAATTTGAGGCTGAGTCCAGTATGATCGTG 357
QY 3530 CTCTACACT-CAGTCTGGGTGACAGTGCAGAAAGCTGTCTCAAAAAATAAATAAATAA 3588
DB 356 CCACTGGACTCCAGCCTGGGTGACAGCAAGACCCCTGTCTCAAAAAAATAAATAAATA 297
QY 3589 AAAA 3592
DB 296 AAAA 293

RESULT 5
US-09-949-016-17403
; Sequence 17403, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20

;	PRIOR APPLICATION NUMBER: 60/237,768	
;	PRIOR FILING DATE: 2000-10-03	
;	PRIOR APPLICATION NUMBER: 60/231,498	
;	PRIOR FILING DATE: 2000-09-08	
;	NUMBER OF SEQ ID NOS: 207012	
;	SOFTWARE: FastSeq for Windows Version 4.0	
;	SEQ ID NO 17403	
;	LENGTH: 17348	
;	TYPE: DNA	
;	ORGANISM: Human	
US-09-949-016-17403		
Query Match	3.3%; Score 186; DB 4; Length 17348;	
Best Local Similarity	74.3%; Pred. No. 1.1e-32;	
Matches	248; Conservative 0; Mismatches 85; Indels 1; Gaps 1;	
Qy	3264 TTTAAATTTTTTAAAAAATAGATGAGTGGTGGCTCATGCTGTAAATCCCAACACTTTT	3323
Db		
Qy	8546 TTTAAAGAGAAAAAATGAGCTGGGCATGGTGGCTCATGCTGTGATGCCAGCACTTT	8605
Db		
Qy	3324 GGAAGCCGGGTCGGGAGGATGACTTTGAGTCAGCAGAGTTTGAGACCAGTCAGGCGCAACAC	3383
Db		
Qy	8606 GAGAGCCAGGCGGAGGATCATTTGAGCCAGGAGTTTGAGCCAGCTGGCCAGAT	8665
Db		
Qy	3384 AGCAAGACCCCATATCTAAAAAACAACAAAAAATAAATTAACCTGGGTATGGTTGCT	3443
Db		
Qy	8666 AGTGAGACCCCTGCTCTACAAAAATAAAAACTTTAAAAAATTAAGCCGGGTGTTGGTGCA	8725
Db		
Qy	3444 CACCTGATCCCAAGCTACACAGGAGCTGAGGCAGAGATCACTTGAGCCAGAGGT	3503
Db		
Qy	8726 CACCTGTAGTCTCAGCTACTCGGAGGCTGAGGCAAGAGATCACTGAGCCCTGGAAGTT	8785
Db		
Qy	3504 TGAGGCTGCAAGTCATCCATGAAGCCGCTGCTACACT-CAGTCTGGGTGACAGTGCAAGAA	3562
Db		
Qy	8786 GGAGGCTGCAGTGAGTATGATGACACATTTGATTCAGCTGGCCAGAGTGAGAC	8845
Db		
Qy	3563 GCTGTCTCAAAAAATAAATAAATAAATAAATAAAC	3596
Db		
Qy	8846 CCTGTCTGTAATTTAAAAAATAAATAAATAAATAAC	8879
Db		
RESULT 6		
US-09-949-016-201827/c		
;	Sequence 201827, Application US/09949016	
;	Patent No. 6812339	
;	GENERAL INFORMATION:	
;	APPLICANT: VENTER, J. Craig et al.	
;	TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED	
;	FILE REFERENCE: CL001307	
;	CURRENT APPLICATION NUMBER: US/09/949,016	
;	FILE REFERENCE: CL001307	
;	CURRENT FILING DATE: 2000-04-14	
;	PRIOR APPLICATION NUMBER: 60/241,755	
;	PRIOR FILING DATE: 2000-10-20	
;	PRIOR APPLICATION NUMBER: 60/237,768	
;	PRIOR FILING DATE: 2000-10-03	
;	PRIOR APPLICATION NUMBER: 60/231,498	
;	PRIOR FILING DATE: 2000-09-08	
;	NUMBER OF SEQ ID NOS: 207012	
;	SOFTWARE: FastSeq for Windows Version 4.0	
;	SEQ ID NO 201827	
;	LENGTH: 601	
;	TYPE: DNA	
;	ORGANISM: Human	
US-09-949-016-201827		
Query Match	3.3%; Score 185.6; DB 4; Length 601;	
Best Local Similarity	74.0%; Pred. No. 3.2e-33;	
Matches	247; Conservative 1; Mismatches 85; Indels 1; Gaps 1;	
Qy	3264 TTTAAATTTTTTAAAAAATAGATGAGTGGTGGCTCATGCTGTAAATCCCAACACTTTT	3323
Db		
Qy	466 TTTAAAGAGAAAAAATGAGCTGGGCATGGTGGCTCATGCTGTGATGGCAGCACTTT	407
Db		

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Db 14781 ATCAGCAGCTGGCTCCAGCTTGGTGACAGTGAGACCTTGCTCTTAAAAAAGAG 14722
QY 3583 TAAATATAAATAAATCTTTTAAAAACAA 3609
Db 14721 AAAAGAAAAAAGAAAAAGAAATGATAA 14695

RESULT 8
US-09-949-016-13444
; Sequence 13444, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 13444
; LENGTH: 172677
; TYPE: DNA
; ORGANISM: Human
US-09-949-016-13444

Query Match 3.3%; Score 184.8; DB 4; Length 172677;
Best Local Similarity 69.6%; Pred. No. 5.3e-32;
Matches 281; Conservative 0; Mismatches 117; Indels 6; Gaps 2;

QY 3195 AAATAACAACTATTGAATCATGACATACGTTTAAATCATATATTAAATACGTGACC 3254
Db 92789 AATTTAAAAATATTACAAAATCATACAAATAGATGTTGAGTTAAATTCATTCAGTTGAC 92848
QY 3255 TATAAACCTTTTAAATTTTTTAAAAAATAGAT-----GAGTGTGGTGGCTCATGCCCTGT 3309
Db 92849 TTTTGTGATTTGGTATTTTTTAAAAAAGATTGACCATGTGTGGTGGCTCGTGTCTGT 92908
QY 3310 AATCCCAACACTTTGGGAAGCGGGTCGGAGGATAGCTTGAGTCCAGCAGTTTGAGACC 3369
Db 92909 AATCCAGCACTTTGGAAGCTGAGTTGCAAGGATAGCTTGAGACCAGGAGTTTGAGACC 92968
QY 3370 AGTCAGGCAACAGCAGCAAGACCCCATATCTAAAAAACAACAAACAAATTTACCTG 3429
Db 92969 AGCTGGGCAACATGGCAAGACCTCATCTACTAAAAAATAAAAAATAAAGCTA 93028
QY 3430 GGTATGTTGTGCTCACCTGTAGTCCAGTACACAGGAAGCTGAGGCAGAGGATCACT 3489
Db 93029 GGCATAGCAGTGTGTTCATATAGTCCAGCTACTCAGAGGCAAGGTTGGAGGATCGCT 93088
QY 3490 TGAGCCCAAGAGGTTGAGGCTGCAGTGATCCATGAACGCGCTGCTPACACT--CAGTCTGGG 3548
Db 93089 TGAACCCAGGAGGTTGAGGCTGCAGTGAGCTGTGATCACACCACTGCACCTCCAGCCTAGG 93148
QY 3549 TGACAGTCACAGAGCTGCTCTCAAAAATAAATAAATAAATAA 3592
Db 93149 TGACAGAGAAAGACCTTGCTCTCAAGAAATAAGCAACAAAAATAA 93192

RESULT 9
US-09-949-016-16949
; Sequence 16949, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 16949
; LENGTH: 33272
; TYPE: DNA
; ORGANISM: Human
US-09-949-016-16949

Query Match 3.3%; Score 184.6; DB 4; Length 33272;
Best Local Similarity 68.6%; Pred. No. 2.9e-32;
Matches 300; Conservative 0; Mismatches 129; Indels 8; Gaps 3;

QY 3170 TTAGCTTAGTAACCTTTAGGATTTTTTAAATAACAACACTATTGAAATCATGACATACGTTTAA 3229
Db 31344 TTGCTTATAAGTTTTTCTCAATATTGTGAAAAAACTTCCACATCGTAGATACATGTCC 31403
QY 3230 ATGATATTATTAAATACGTTTAGGCTATATAAACCTTTTAAATTTTTTAAAAAATATAGTGA 3289
Db 31404 ATAAATTTTTTTTGTATTGTTTGTGATTTTAA--TTAAATTTTATTGAAATATAGCTGG 31460
QY 3290 GTGTGGTGGCTCATGCCCTGTAATCCAAACACTTTTGGGAAGCGGGTCGGAGGATAGCTT 3349
Db 31461 GTGCAGTGGCTTACCTCTGTAAATCCCAACACTTTTGAGAGGCTGAGTGGGATGATTCCTT 31520
QY 3350 GAGTCCACAGCTTTGAGACCACTGAGGCAAGCAACAGCAAGACCCCATATCTAAAAAACA 3409
Db 31521 GAGTCCAGGAGTTCAAGACCACTTGGGCAACACAGCAGATACATCTCTTCAAAAAA 31580
QY 3410 AAACAAACAAATTTACCTGGGTATGTTGTCTCACCTGAGTCCAAAGCTACACAGGAA 3469
Db 31581 ATAGA---AAAATAGCTGGGCATGGTGGCTGTGTAGTCCAGCTACTCGGAG 31636
QY 3470 GCTGAGCAGAAAGCATCTTTCAGCCAGGAGGTTGAGGCTGCAGTGCATGATCAACCGG 3529
Db 31637 GCTGAGCGGGGGGATCACTTTGAGCCAGGAGGTTGAGGCTGCAGTGCATGATGATGCA 31696
QY 3530 CTGCTACACT--CAGTCTGGGTGACAGTGCAAGAGAGCTCTCTCAAAAAATAAATAAATA 3588
Db 31697 CTGTGCACTCCAGGTTGGGTGACAGAGCAAGACCTGTCTCAAAAACCCCAAAAAACA 31756
QY 3589 AAAATAAATTTTAAAAA 3605
Db 31757 AACTGAAATATCAATA 31773

RESULT 10
US-09-949-016-58699
; Sequence 58699, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
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; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 16949
; LENGTH: 33272
; TYPE: DNA
; ORGANISM: Human
US-09-949-016-16949

Query Match 3.3%; Score 184.6; DB 4; Length 33272;
Best Local Similarity 68.6%; Pred. No. 2.9e-32;
Matches 300; Conservative 0; Mismatches 129; Indels 8; Gaps 3;

QY 3170 TTAGCTTAGTAACCTTTAGGATTTTTTAAATAACAACACTATTGAAATCATGACATACGTTTAA 3229
Db 31344 TTGCTTATAAGTTTTTCTCAATATTGTGAAAAAACTTCCACATCGTAGATACATGTCC 31403
QY 3230 ATGATATTATTAAATACGTTTAGGCTATATAAACCTTTTAAATTTTTTAAAAAATATAGTGA 3289
Db 31404 ATAAATTTTTTTTGTATTGTTTGTGATTTTAA--TTAAATTTTATTGAAATATAGCTGG 31460
QY 3290 GTGTGGTGGCTCATGCCCTGTAATCCAAACACTTTTGGGAAGCGGGTCGGAGGATAGCTT 3349
Db 31461 GTGCAGTGGCTTACCTCTGTAAATCCCAACACTTTTGAGAGGCTGAGTGGGATGATTCCTT 31520
QY 3350 GAGTCCACAGCTTTGAGACCACTGAGGCAAGCAACAGCAAGACCCCATATCTAAAAAACA 3409
Db 31521 GAGTCCAGGAGTTCAAGACCACTTGGGCAACACAGCAGATACATCTCTTCAAAAAA 31580
QY 3410 AAACAAACAAATTTACCTGGGTATGTTGTCTCACCTGAGTCCAAAGCTACACAGGAA 3469
Db 31581 ATAGA---AAAATAGCTGGGCATGGTGGCTGTGTAGTCCAGCTACTCGGAG 31636
QY 3470 GCTGAGCAGAAAGCATCTTTCAGCCAGGAGGTTGAGGCTGCAGTGCATGATCAACCGG 3529
Db 31637 GCTGAGCGGGGGGATCACTTTGAGCCAGGAGGTTGAGGCTGCAGTGCATGATGATGCA 31696
QY 3530 CTGCTACACT--CAGTCTGGGTGACAGTGCAAGAGAGCTCTCTCAAAAAATAAATAAATA 3588
Db 31697 CTGTGCACTCCAGGTTGGGTGACAGAGCAAGACCTGTCTCAAAAACCCCAAAAAACA 31756
QY 3589 AAAATAAATTTTAAAAA 3605
Db 31757 AACTGAAATATCAATA 31773

RESULT 10
US-09-949-016-58699
; Sequence 58699, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
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[illegible]

QY	3323	TGGGAAGCCGGGTGCGGAGATAGCTTGAGTCCAGCAGTTTCAGACCACTTCAGGCCAACA	3382
Db	227	TGGGAGGCCGAGGTGGGTGGATCACTTGAGGCCAGGATTTCGAGACCACCTGGGTGACA	286
QY	3383	CAGCAAGACCCCATATCTAAAAAAACAAAACAAAATTAACCTGGGTATGTTGTGC	3442
Db	287	TAGTCAGATCTTTGTTCTGCAAAAAAAAATAATGTTTTAAATCAGCCAGGTGGTGGTGC	346
QY	3443	TCACCTGTAGTCCAAGCTACACAGGAAGCTGAGGCAGAGGATCACTTCAGCCCCAGGAGG	3502
Db	347	CTGCCCTGTAGTTTCAGATACTCGAGAGGCTAAGGTGGAAAGGATTGCTTCAGTCCAGGAGT	406
QY	3503	TTGAGGCTGCAGTGTATCCATGAACGGCTGTCTACACT--CAGTCTGGGTGACAGTCCAAG	3560
Db	407	TTGAGGCTGCAGTAGCTATGATCATGCCATTGCAGTTCAGCTTTGGGTGACAGAGCAAG	466
QY	3561	AAGCTGTCTCAAAAAATAAATAAATAAAAAATACTTTTAAAAAACAAAAATTAATTAA	3620
Db	467	ACCCGTGCTCAACAAAAACACAGAAGTAGTATATGATATATAGTCCAGGTATTATTTA	526
QY	3621	ATTTTAAAA	3629
Db	527	ACAGTAATA	535

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RESULT 13
US-09-949-016-12256/c
; Sequence 12256, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 12256
; LENGTH: 36228
; TYPE: DNA
; ORGANISM: Human
US-09-949-016-12256

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[illegible]

Qy	3495	CCAGGAGGTTGAGGCTGCAGTGTATCCATGAACGCGCTGTCTACACT-CAGTCTGGGTGACA	3553
Db	6882	CCGGAGGCAGAGGTTGCAGTGAGCGCAAGATCACGCCGTTGCACCTCCAGCCAGGCGACA	6923
Qy	3554	GTGCAAGAAGCTGTCTCAAAATATAAATAAATAAATACTTTTAAAAACAACAAAAT	3613
Db	6922	GAGCAAAACTCCATCTCAAAAATAAAAAAATAAAAAAAGAAAAATGAAAAAGACAAAC	6763
Qy	3614	TAAATTAATTTTAAAAACACACACACTAGAGATGTTTGGCAAATTTGATTATTGGGAGTC	3673
Db	6762	TCAATGATAGGATAAAATATTTTGGCAATCATATATCTGATAAGGACCCTGTATCTAGAA	6703
Qy	3674	TATATCCCTGGAAGTTAAATTTAAAAATATTTAGAAGA	3709
Db	6702	TATAAAAAGAAATCTTGTAACTCAATAATAAGAAGA	6667

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RESULT 14
US-09-949-016-15468/c
; Sequence 15468, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 15468
; LENGTH: 36228
; TYPE: DNA
; ORGANISM: Human
US-09-949-016-15468

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[illegible]

Db 6822 GAGCAAACTCCATCTCAAAAAAAAAAAAAAAAAAAAAAAAAAGAAAAATGAAAAAGACAAC 6763
Qy 3614 TAATTAATTTTAAAAACACACACTAGAGATGTTTGCRAATTGATTATTTGGGAGTC 3673
Db 6762 TCAATGAATAGGATAAATAATTTGCAATCATATATCTGATAAGGACCTGTATCTAGAA 6703
Qy 3674 TATATCCCTGGAAGTTAATTTAAAAATATTTAGAAGA 3709
Db 6702 TATAAAGAATCTTGTAACTCAATATAGAAGA 6667

RESULT 15
US-09-949-016-12672/c
; Sequence 12672, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 12672
; LENGTH: 134140
; TYPE: DNA
; ORGANISM: Human
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (1)..(134140)
; OTHER INFORMATION: n = A, T, C or G
US-09-949-016-12672

Query Match 3.2%; Score 182.6; DB 4; Length 134140;
Best Local Similarity 64.4%; Pred. No. 1.5e-31;
Matches 289; Conservative 0; Mismatches 159; Indels 1; Gaps 1;
Qy 3268 AATTTTAAATAATAGATGAGTGGTGCTCATGCTTAATCCCAACTTTGGGA 3327
Db 94152 AAAATGTACAAGAAATATATGCGCGGTGTAGTGATGCTGTAAATCCAGCACTTAGGA 94093
Qy 3328 AGCCGGGTGGGAGGATAGCTTCAGTCCAGAGTTTGAGACCACTCAGGGCAACACAGCA 3387
Db 94092 AGCCAAGATGGGAGTATCACTTAAGCCAGGAGTTTCAGGATCAGCCTAGACAACTGGAG 94033
Qy 3388 AGACCCCATATCTAAAAAACAACAAACAAATACCTGGGTATGGTTGCTCACC 3447
Db 94032 AAATCCTCTCTACAAAAACAAAAAATACAAAAATTTAGCTGGGTGTGATGGTACACGCC 93973
Qy 3448 TGTAGTCCAGCTACACAGGAAGCTGAGGAGGATCACTTGAGCCAGGAGTTGAG 3507
Db 93972 TGTAGTCCAGCTACTTAGGAGCTGAAGTGGGAGGATCACTTGAGCCAGGAGTTGAG 93913
Qy 3508 GCTGCAGTGATCCATGAACCGGTGCTACACTC-AGTCTGGGTGACAGTGCAGAAAGCTG 3566
Db 93912 ACTGCAGTGATCCATGATTGTGCCACTGCACTCTAGCCTTGGTGACACAATAAGACCTG 93853
Qy 3567 TCTCAAAAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAA 3626
Db 93852 TTTCCAAAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAA 93793
Qy 3627 AAACACACACACTAGAGATGTTGCAATTTGATTTTGGGAGTCTATATCCTCGAA 3686
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Job time : 857 secs

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

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(without alignments)

11540.627 Million cell updates/sec

Title: US-10-030-294-1

Perfect score: 5676

Sequence: 1 cagctgttcaggatgctcg.....tttataattgttcccg 5676

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Gapop 10'0 , Gapext 1.0

Searched: 9784742 seqs, 4129495052 residues

Total number of hits satisfying chosen parameters: 19569484

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

Published Applications NA:*

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22: /cgn2_6/ptodata/1/pubpna/US10I_PUBCOMB.seq:*
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26: /cgn2_6/ptodata/1/pubpna/US11_NEW_PUB.seq:*
27: /cgn2_6/ptodata/1/pubpna/US60_NEW_PUB.seq:*
28: /cgn2_6/ptodata/1/pubpna/US60_PUBCOMB.seq:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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1	632.6	11.1	633	13	US-09-925-065A-842014
C 2	196.2	3.5	65793	22	Sequence 842014, Sequence 3, Appli
C 3	196	3.5	304905	19	Sequence 1, Appli
4	193.8	3.4	536	13	US-10-030-294-1
5	193	3.4	13070	22	US-09-925-065A-552295
					Sequence 17605, A

C	6	193	3.4	156318	22	US-10-741-600-17574	Sequence 17574, A
7	192.2	3.4	536	13	US-09-925-065A-552294	Sequence 552294, A	
8	188.4	3.3	135005	21	US-10-723-860-2320	Sequence 2320, Ap	
9	188.4	3.3	135005	24	US-10-756-149-1719	Sequence 1719, Ap	
10	187.6	3.3	8133	19	US-10-380-124-10	Sequence 10, Appl	
C 11	186	3.3	587	13	US-09-925-065A-123687	Sequence 123687, A	
C 12	186	3.3	18861	11	US-09-984-429-513	Sequence 513, App	
C 13	185.6	3.3	606	13	US-09-925-065A-901413	Sequence 901413, A	
C 14	185.6	3.3	610	13	US-09-925-065A-907871	Sequence 907871, A	
C 15	185.6	3.3	611	14	US-10-027-632-181221	Sequence 181221, A	
C 16	185.6	3.3	611	18	US-10-027-632-181221	Sequence 181221, A	
C 17	185.4	3.3	3287	14	US-10-027-632-115440	Sequence 115440, A	
C 18	185.4	3.3	3287	18	US-10-027-632-115440	Sequence 115440, A	
C 19	185.4	3.3	47999	24	US-10-477-720A-4	Sequence 4, Appli	
C 20	184.4	3.2	587	13	US-09-925-065A-123685	Sequence 123685, A	
C 21	184.4	3.2	587	13	US-09-925-065A-123686	Sequence 123686, A	
C 22	183	3.2	335199	22	US-10-496-011-4	Sequence 4, Appli	
C 23	182.6	3.2	615	13	US-09-925-065A-916797	Sequence 916797, A	
C 24	182.6	3.2	47903	20	US-10-322-281-808	Sequence 808, App	
25	182.4	3.2	736	14	US-10-027-632-17813	Sequence 17813, A	
26	182.4	3.2	736	18	US-10-027-632-17813	Sequence 17813, A	
27	182.2	3.2	36651	9	US-09-964-469-3	Sequence 3, Appli	
28	182.2	3.2	36651	17	US-10-425-962-3	Sequence 3, Appli	
29	182	3.2	570	13	US-09-925-065A-517201	Sequence 517201, A	
30	182	3.2	570	13	US-09-925-065A-517202	Sequence 517202, A	
31	182	3.2	55735	22	US-10-741-600-17698	Sequence 17698, A	
C 32	181.8	3.2	728	13	US-09-925-065A-918286	Sequence 918286, A	
C 33	181.8	3.2	728	13	US-09-925-065A-918287	Sequence 918287, A	
C 34	181.8	3.2	50000	18	US-10-364-505-8	Sequence 8, Appli	
C 35	181.8	3.2	50000	20	US-10-681-199-8	Sequence 8, Appli	
C 36	181.4	3.2	728	13	US-09-925-065A-918288	Sequence 918288, A	
37	181.4	3.2	145806	21	US-10-719-993-6943	Sequence 6943, Ap	
38	181.2	3.2	113589	24	US-10-764-425-9	Sequence 9, Appli	
39	181	3.2	576	13	US-09-925-065A-731417	Sequence 731417, A	
C 40	181	3.2	615	13	US-09-925-065A-895987	Sequence 895987, A	
41	181	3.2	615	13	US-09-925-065A-895987	Sequence 895987, A	
42	181	3.2	683	13	US-09-925-065A-709225	Sequence 709225, A	
43	181	3.2	683	13	US-09-925-065A-709226	Sequence 709226, A	
44	181	3.2	683	13	US-09-925-065A-709227	Sequence 709227, A	
45	181	3.2	58985	10	US-09-901-152-3	Sequence 3, Appli	
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ALIGNMENTS

RESULT 1

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US-09-925-065A-842014
; Sequence 842014, Application US/0925065A
; Publication No. US20050228172A9
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide Polymorphisms in the Human Genome
; FILE REFERENCE: 108927.135
; CURRENT APPLICATION NUMBER: US/09/925,065A
; PRIOR FILING DATE: 2001-08-08
; PRIOR FILING DATE: 2000-10-24
; PRIOR FILING DATE: 2000-10-24
; PRIOR FILING DATE: 2000-11-20
; PRIOR FILING DATE: 2000-11-20
; PRIOR FILING DATE: 2000-11-30
; PRIOR FILING DATE: 2000-11-30
; PRIOR FILING DATE: 2001-01-16
; PRIOR FILING DATE: 2001-01-16
; PRIOR FILING DATE: 2001-05-09
; NUMBER OF SEQ ID NOS: 957086
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 842014
; LENGTH: 633
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-925-065A-842014
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Query Match 11.1%; Score 632.6; DB 13; Length 633;
Best Local Similarity 99.8%; Pred. No. 2.2e-123;
Matches 632; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

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DB 1 AGCAAACTCTTTAACTGCAATTAACAAATCTATAATTAATTAAGTTAAGCAATCTTCCCT 60

QY 4124 TTAAGTTTACATTTTGTGGCAAGCTGTTGATTTGGCTGGGCTCAGCGCGCTGT 4183
DB 61 TTAAGTTTACATTTTGTGGCAAGCTGTTGATTTGGCTGGGCTCAGCGCGCTGT 120

QY 4184 TTGTGAATTCACAAATTCACAGATGTAGCGCTCTCGGCTTAAGTAAGGAAGAGATG 4243
DB 121 TTGTGAATTCACAAATTCACAGATGTAGCGCTCTCGGCTTAAGTAAGGAAGAGATG 180

QY 4244 TCAAGTTTAAATAGCTTCTCCCTCCATCTCGCTGAAGCAAAATAAATATTTTAA 4303
DB 181 TCAAGTTTAAATAGCTTCTCCCTCCATCTCGCTGAAGCAAAATAAATATTTTAA 240

QY 4304 TGAACACATTTTGTAGTTAGATTTACTTACAGGAAATGTCAAATTTCTCTGAAGGGCT 4363
DB 241 TGAACACATTTTGTAGTTAGATTTACTTACAGGAAATGTCAAATTTCTCTGAAGGGCT 300

QY 4364 TTAGATTGCTCACAATTTGACATCTACTGATGTCACTTATTTACAGGTGTCTCTGTG 4423
DB 301 TTAGATTGCTCACAATTTGACATCTACTGATGTCACTTATTTACAGGTGTCTCTGTG 360

QY 4424 ACTAGGGGTGAAGGAAGATGTGAATCACTACCACTGTAGTGACCGTTAGATACACAGAT 4483
DB 361 ACTAGGGGTGAAGGAAGATGTGAATCACTACCACTGTAGTGACCGTTAGATACACAGAT 420

QY 4484 GGTGTTTTTCCCTGTTGGAGTCTATCTAACTGAGCTTCTGAATCATATTTCAATCA 4543
DB 421 GGTGTTTTTCCCTGTTGGAGTCTATCTAACTGAGCTTCTGAATCATATTTCAATCA 480

QY 4544 ATTTCCAAATCCAAACACGATAGTTTACAGCCCATTTACAGGAAGGAATTAAT 4603
DB 481 ATTTCCAAATCCAAACACGATAGTTTACAGCCCATTTACAGGAAGGAATTAAT 540

QY 4604 ATTTGTGTAGACTTCTCGATATTTACACTGATTTGGGAATATATGAACATTTTATG 4663
DB 541 ATTTGTGTAGACTTCTCGATATTTACACTGATTTGGGAATATATGAACATTTTATG 600

QY 4664 GTTTCCTTCGAAAGTAGGTCAGTCAAAGCAAA 4696
DB 601 GTTTCCTTCGAAAGTAGGTCAGTCAAAGCAAA 633

RESULT 2
US-10-703-817-3/c
; Sequence 3, Application US/10703817
; Publication No. US20050118117A1
; GENERAL INFORMATION:
; APPLICANT: ROTH, RICHARD B.
; APPLICANT: NELSON, MATTHEW ROBERTS
; APPLICANT: KAMMERER, STEFAN M.
; APPLICANT: BRAUN, ANDREAS
; TITLE OF INVENTION: METHODS FOR IDENTIFYING RISK OF MELANOMA AND TREATMENTS
; TITLE OF INVENTION: THEREOF
; FILE REFERENCE: SEQ-4061-UT
; CURRENT APPLICATION NUMBER: US/10/703,817
; CURRENT FILING DATE: 2003-11-06
; PRIOR APPLICATION NUMBER: 60/489,703
; PRIOR FILING DATE: 2003-07-23
; PRIOR APPLICATION NUMBER: 60/424,475
; PRIOR FILING DATE: 2002-11-06
; NUMBER OF SEQ ID NOS: 255
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 3
; LENGTH: 65793
; TYPE: DNA

; ORGANISM: Homo sapiens
US-10-703-817-3

Query Match 3.5%; Score 196.2; DB 22; Length 65793;
Best Local Similarity 70.0%; Pred. No. 5.4e-30;
Matches 278; Conservative 0; Mismatches 118; Indels 1; Gaps 1;

QY 3262 CTTTAAATTTTTTAAAAAATAGATGAGTGTGGTGGCTCATGCTGTATATCCACACT 3321
DB 18059 CTATAAAGTTTTTACAGGAAAGCCAGGTGCGGTGCACACCTGTATATCCACACT 18000

QY 3322 TTGGGAAGCCGGTGGGAGGATAGCTTGAGTCCAGCAGTTTGAGACCACTGAGGGCAAC 3381
DB 17999 TTGGGAGCTGAGGAGGAGTGGATTTGCTGAGCTCAGGAGTTTGAGACCACTGAGGGCAAC 17940

QY 3382 ACAGCAAGACCCCATATCTAAAAAACAACAAAAAATACTCTGGGTATGTTGTG 3441
DB 17939 ATGGCAAAACCCATCTCTACATAAAATACAGAAAAAATAATAGCTGGTGGTG 17880

QY 3442 CTCACCTGTAGTCCAAGCTACACAGAAAGCTCAGGCAAGGATCACTTTGAGCCCAAG 3501
DB 17879 CACACCTGTGGTCTGCTTACTCAGGAGTCTCAGATGGGAGGATTCCTTGAGCCCAAG 17820

QY 3502 GTTGAGGCTGCACTGATCCATGAACGCGCTGCTACACT-CAGTCTGGGTGACAGTGCAG 3560
DB 17819 ATTGAGCTGCACTGAGTCCAGATCATGCCACTGTACTCCAGCTGGGCAACAGAGCAAG 17760

QY 3561 AAGCTGTCTCAAAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAA 3620
DB 17759 ACTCCATCTCAAAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATA 17700

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DB 17699 TATAATATATACACACACTATATTATGTATATAT 17663

RESULT 3
US-10-271-416-1/c
; Sequence 1, Application US/10271416
; Publication No. US20040043021A1
; GENERAL INFORMATION:
; APPLICANT: Keith, Tim
; APPLICANT: Little, Randall D.
; APPLICANT: Van Berdewegh, Paul
; APPLICANT: Dupuis, Josee
; APPLICANT: Del Mastro, Richard G.
; APPLICANT: Allen, Kristina
; TITLE OF INVENTION: NUCLEOTIDE AND AMINO ACID SEQUENCES
; TITLE OF INVENTION: RELATING TO RESPIRATORY DISEASES AND OBESITY
; FILE REFERENCE: 2976-4045
; CURRENT APPLICATION NUMBER: US/10/271,416
; CURRENT FILING DATE: 2002-10-11
; PRIOR APPLICATION NUMBER: 60/328,424
; PRIOR FILING DATE: 2001-10-11
; NUMBER OF SEQ ID NOS: 9
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 304905
; TYPE: DNA
; ORGANISM: Homo sapien
US-10-271-416-1

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Best Local Similarity 73.3%; Pred. No. 1.3e-29;
Matches 264; Conservative 0; Mismatches 95; Indels 1; Gaps 1;

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DB 156005 AATCTCGTGGGTGGGTAGCTCACCTGTATATCCAGCAGCTTTGGGAGCCAGGTGG 155946

QY 3339 GAGGATAGCTTCAGTCCAGCAGTTTGAGACCACTGAGGCAACAGAGCAAGACCCCATAT 3398
DB 155945 GAGGATTTGCTTAAGCCCAAGGAGTTTGAGACCACTGAGGCAACAGTGTGAAACCCCATGT 155886

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QY	3519	CCATGAACCGCTGCTACACT-CAGTCTGGGTGACAGTGCAGAGAAGCTGTCTCAAAAAATA	3577
Db	155765	TGCTGATCGCGCACTGCATCTCCAGCTGGGTGACAGAGTAAGACCCCGTCTCAAAAAA	155706
QY	3578	ATAAATAAATAAAATACTTTTAAAAAACAAAAATTAATTAAATTTTAAAAACAACA	3637
Db	155705	AAAAAATAAAACAAACACCAGAAACTCAATCTCTCTCTCTTTAAAAAAGCA	155646
RESULT 4			
US-09-925-065A-552295			
; Sequence 552295, Application US/09925065A			
; Publication No. US2005028172A9			
; GENERAL INFORMATION:			
; APPLICANT: wang, David G.			
; TITLE OF INVENTION: Identification and Mapping of Single			
; FILE OF INVENTION: Nucleotide Polymorphisms in the Human Genome			
; FILE REFERENCE: 108827.135			
; CURRENT APPLICATION NUMBER: US/09/925,065A			
; CURRENT FILING DATE: 2001-08-08			
; PRIOR APPLICATION NUMBER: US 60/243,096			
; PRIOR FILING DATE: 2000-10-24			
; PRIOR APPLICATION NUMBER: US 60/252,147			
; PRIOR FILING DATE: 2000-11-20			
; PRIOR APPLICATION NUMBER: US 60/250,092			
; PRIOR FILING DATE: 2000-11-30			
; PRIOR APPLICATION NUMBER: US 60/261,766			
; PRIOR FILING DATE: 2001-01-16			
; PRIOR APPLICATION NUMBER: US 60/289,846			
; PRIOR FILING DATE: 2001-05-09			
; NUMBER OF SEQ ID NOS: 957086			
; SOFTWARE: FastSeq for Windows Version 4.0			
; SEQ ID NO 552295			
; LENGTH: 536			
; TYPE: DNA			
; ORGANISM: Homo sapiens			
US-09-925-065A-552295			
Query Match 3.4%; Score 193.8; DB 13; Length 536;			
Best Local Similarity 70.9%; Pred. No. 1.6e-30;			
Matches 270; Conservative 1; Mismatches 108; Indels 2; Gaps 1;			
QY	3212	ATCATGACATACGTTTAAATGATATTATTAAATACGTTTAGGCTATAAACCTTTTAAATT	3271
Db	1	ATCTGTACAAAACATCTGATTTTCAATTTTAAAGTTAAAGTTAAATCTTA	60
QY	3272	TTTTAAAAAATAGATGAGTGTGGTGGCTCATGCTGTAAATCCCAACACTTTGGGAAGCC	3331
Db	61	RAAGTCAAAGATTGCTGGGTATGGTAGCTCAGCCTGTAATTTCAAACACTCTAGGAGCC	120
QY	3332	GCGTCGGAGGATAGTTGAGTCCAGACGATTTGAGACCGAGTCCAGGCAACACAGCAAGAC	3391
Db	121	GAGGCGGGCGTATCGTTGAGCCCGGGGTTTGAACACAGTCTAGGCGCAACAGGCAAAAC	180
QY	3392	CCCATATCTTAAAAAACAACAAAAAATACTCGGTATGGTTGCTCCTCCTCTGA	3451
Db	181	CCCATCTCTTACAAAATAAAAATACA--ATAATGAGCTGGGCATGGTGGCAGCAGCTGTG	238
QY	3452	GTCCAAGCTTACACAGGAAGCTGAGGAGAGGATCACTTTGAGCCCCAGGAGTTGAGGCTG	3511
Db	239	GTCCAGCTACTTTGGAGGCTGAGGAGAGGATGGCTTGAGCCCNAGAKGTTGGGCTG	298
QY	3512	CAGTGATCATGAACGCGCTGCTTACACTCAGTCTCGGTGACAGTGCAGAGCTGTCTCA	3571

Db 299 CAGTGAGCTGTGACTGTACTACTCCACTAGGTGACAGATAAGACCCCTGTCTCA 358

Qy 3572 AAAATAATAATAATAAAAA 3592
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Db 359 AAAATAAACAAATAAAAAATAA 379

RESULT 5

US-10-741-600-17605

; Sequence 17605, Application US/10741600

; Publication No. US20050026169A1

; GENERAL INFORMATION:

; APPLICANT: CARGILL, Michele et al.

; TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH

; FILE REFERENCE: CL001499

; CURRENT APPLICATION NUMBER: US/10741.600

; CURRENT FILING DATE: 2003-12-22

; NUMBER OF SEQ ID NOS: 73997

; SOFTWARE: FastSeq for Windows Version 4.0

; SEQ ID NO 17605

; LENGTH: 13070

; TYPE: DNA

; ORGANISM: Homo sapiens

US-10-741-600-17605

Query Match 3.4%; Score 193; DB 22; Length 13070;

Best Local Similarity 70.8%; Pred. No. 1.1e-29;

Matches 271; Conservative 0; Mismatches 110; Indels 2; Gaps 1;

Qy 3310 AAATCATGACATACGTTTAAATGATATATTTAAATACGTTAGGCTATAAACCCTTTTAAA 3269

Db 10423 ATATCTGTACAAAACATCTGATTTTCACTTTTCAAAATCTTTAGGTAGTAAAGTTAAAAATC 10482

Qy 3270 TTTTAAAAAATAGATGAGTGTGGCTCATGCCCTGTAATCCCAACACTTTTCGGGAAG 3329

Db 10483 TAAAGTCAAGATTGCTGGGTATGGTAGCTCAGCCCTGTAAATCCACACTCTAGGAGG 10542

Qy 3330 CCGGGTCGGGAGGTAGCTTTGAGTCCAGCAGTGTGAGACCCAGTTCAGGGCAACACAGCAAG 3389

Db 10543 CCGAGGCGGCATATCGCTTGAGCCAGGGGTTTGAGACCAGCTAGGGCAACAGGCAAA 10602

Qy 3390 ACCCATATCTAAAAAACAACAAACAAATAATACCTGGGTATGGTTGTGCTCACCTG 3449

Db 10603 ACCCATCTCTACAAAAATAAAATACAA--ATAATGAGCTGGGCATGGTGCGCACGACCTG 10660

Qy 3450 TAGTCCAGCTACACAGGAGCTCAGCAGAGAGGATCACTTGAGCCAGGAGTTTGAGGC 3509

Db 10661 TGGTCCAGCTACTTGGGAGGCTGAGGAGGAGGATGGCTTGAGCCAGGAGTTTGGGCG 10720

Qy 3510 TGCAGTGATCCATGAACCGCTGCTACACTCAGTCTGGGTGACAGTGCAGAGAGCTGTCT 3569

Db 10721 TGCAGTGAGCTGTGACTGTACTCTGCACCTCCACTAGTGCACAGAATAAGACCCCTGTCT 10780

Qy 3570 CAAAAATAATAATAATAAAAA 3592

Db 10781 CAAAAATAAACAAATAAAAAATAA 10803

RESULT 6

US-10-741-600-17574/c

; Sequence 17574, Application US/10741600

; Publication No. US20050026169A1

; GENERAL INFORMATION:

; APPLICANT: CARGILL, Michele et al.

; TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH

; FILE REFERENCE: CL001499

; CURRENT APPLICATION NUMBER: US/10741.600

; CURRENT FILING DATE: 2003-12-22

; NUMBER OF SEQ ID NOS: 73997

; SOFTWARE: FastSeq for Windows Version 4.0

; SEQ ID NO 17574

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RESULT 6
US-10-741-600-17574/c
; Sequence 17574, Application US/10741600
; Publication No. US20050026169A1
; GENERAL INFORMATION:
; APPLICANT: CARGILL, Michele et al.
; TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
; TITLE OF INVENTION: MYOCARDIAL INFARCTION, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001499
; CURRENT APPLICATION NUMBER: US/10/741.600
; CURRENT FILING DATE: 2003-12-22
; NUMBER OF SEQ ID NOS: 73997
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 17574

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; LENGTH: 156318
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)...(156318)
; OTHER INFORMATION: n = A,T,C or G, or insertion/deletion polymorphism (see Tables 1-
US-10-741-600-17574

Query Match          3.4%; Score 193; DB 22; Length 156318;
Best Local Similarity 70.8%; Pred. No. 4e-29;
Matches 271; Conservative 0; Mismatches 110; Indels 2; Gaps 1;

QY 3210 AAATCATGACATACGTTTAAATGATATTTTAAATACGTTAGCTATTAACCTTTTAAA 3269
Db 66635 ATATCTGTACAAACATCTGATTCACCTTTTCAAATCTTTAGTAGTAAAGTTAAATC 66576

QY 3270 TTTTAAATAAATAGATGAGTGTGGTGTCTATGCTGTAATCCCAACATTTGGGAAG 3329
Db 66575 TAAAGGTCAAAGATTGCTGGGTATGGTAGCTCAGGCTGTAAATTCCAACACTCTAGGAG 66516

QY 3330 CCGGTCGAGGAGTACGTGAGTCCAGCAGTTTGAGACCAGTCAGGGGCAACACAGAAG 3389
Db 66515 CCGAGCGGGCATATCGCTTGAGCCCGAGGGGTTTGAGACCAGTCCAGGCAACAGGCAAA 66456

QY 3390 ACCCCATATCTAAATAAACAACAAACAAACAAATTAACCTGGGTATGTTGTCTCACTG 3449
Db 66455 ACCCATCTCTACAAATAAATAACA--ATAATGAGCTGGGCATGTGGCAGCACCTG 66398

QY 3450 TAGTCAAGCTACACAGGAAGCTGAGGCAGAGGATCACTTGAGCCAGGAGGTTGAGGC 3509
Db 66397 TGGTCCAGCTACTTGGAGGCTGAGGCAGGAGGATGGCTTGAGCCAGGAGGTTGGGC 66338

QY 3510 TGCAGTGATCCATGAAGCGCTCTACACTCAGTCTGGGTGACAGTGCAAGAGCTGTCT 3569
Db 66337 TGCAGTGAGCTGAGCTGACTACTACTCAGTCTCCACCTAGGTGACAGAAATAGACCCCTGTCT 66278

QY 3570 CAAAAATAAATAAATAAATAA 3592
Db 66277 CAAAAATAAATAAATAAATAA 66255

RESULT 7
US-09-925-065A-552294
; Sequence 552294, Application US/09925065A
; Publication No. US20050228172A9
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single
; FILE OF INVENTION: Nucleotide Polymorphisms in the Human Genome
; FILE REFERENCE: 108827.135
; CURRENT APPLICATION NUMBER: US/09/925,065A
; CURRENT FILING DATE: 2001-08-08
; PRIOR APPLICATION NUMBER: US 60/243,096
; PRIOR FILING DATE: 2000-10-24
; PRIOR APPLICATION NUMBER: US 60/252,147
; PRIOR FILING DATE: 2000-11-20
; PRIOR APPLICATION NUMBER: US 60/250,092
; PRIOR FILING DATE: 2000-11-30
; PRIOR APPLICATION NUMBER: US 60/261,766
; PRIOR FILING DATE: 2001-01-16
; PRIOR APPLICATION NUMBER: US 60/289,846
; PRIOR FILING DATE: 2001-05-09
; NUMBER OF SEQ ID NOS: 957086
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 552294
; LENGTH: 536
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-925-065A-552294

Query Match          3.4%; Score 192.2; DB 13; Length 536;
Best Local Similarity 70.6%; Pred. No. 3.4e-30;
Matches 269; Conservative 1; Mismatches 109; Indels 2; Gaps 1;

QY 3212 ATCATGACATACGTTTAAATGATATTTTAAATACGTTAGGCTATAAACCTTTTAAAT 3271
Db 1 ATCTGTACAAACATCTGATTTTCACTTTTCAAAATCTTTTAGGTAGTAAAGTTAAATCTTA 60

QY 3272 TTTTAAATAAATAGATGAGTGTGGTGTCTATGCTGTAAATCCCAACACTTTGGGAAGCC 3331
Db 61 AAGGTCAAAGATTGCTGGGTATGGTAGCTCAGCCTGTAAATCCCAACACTCTAGGAGGCC 120

QY 3332 GGGTGGGAGGATAGCTTGGTCCAGCAGTTTGAGACCAGTCAAGGCAACACAGCAAGAC 3391
Db 121 GAGGGGGGRTATCGCTTGAGCCAGGGGTTTGAGACCAGTCAAGGCAACAGGCAAAAC 180

QY 3392 CCCATATCTAAATAAACAACAAACAAACAAATTAACCTGGGTATGGTGTGCTCACCTGTA 3451
Db 181 CCATCTCTACAAATAAATAAATAACA--ATAATGAGCTGGGCATGTGGCAGCAGCCTGTG 238

QY 3452 GTCCAAGCTACACAGGAAGCTGAGGCAGAAAGATCACTTTGAGCCCAAGGAGTTTGAGGCTG 3511
Db 239 GTCCAGCTACTTGGGAGGCTGAGGCAGGAGGATGGCTTGAGCCCAAGGATGTGGGCTG 298

QY 3512 CAGTGATCATGAACCGCTGCTACACTCAGTCTGGGTGACAGTGCAGAAAGCTGTCTCA 3571
Db 299 CAGTGAGCTGTGACTGTACTACTGCACTCCACTAGTGTGACAGAAATAAGACCTGTCTCA 358

QY 3572 AAAAAATAAATAAATAAATAA 3592
Db 359 AAAAAATAAATAAATAAATAA 379

RESULT 8
US-10-723-860-2320
; Sequence 2320, Application US/10723860
; Publication No. US20040253606A1
; GENERAL INFORMATION:
; APPLICANT: Aziz, Natasha
; APPLICANT: Ginsburg, Wendy M.
; APPLICANT: Zlotnik, Albert
; TITLE OF INVENTION: Methods of Diagnosis of Soft Tissue Sarcoma, Compositions &
; FILE OF INVENTION: Methods for Screening for Soft Tissue Sarcoma Modulators
; FILE REFERENCE: 05882.0193.NPUS01
; CURRENT APPLICATION NUMBER: US/10/723,860
; CURRENT FILING DATE: 2003-11-26
; PRIOR APPLICATION NUMBER: 60/429,739
; PRIOR FILING DATE: 2002-11-26
; NUMBER OF SEQ ID NOS: 8393
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 2320
; LENGTH: 135005
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-723-860-2320

Query Match          3.3%; Score 188.4; DB 21; Length 135005;
Best Local Similarity 71.8%; Pred. No. 3.5e-28;
Matches 260; Conservative 0; Mismatches 101; Indels 1; Gaps 1;

QY 3263 TTTTAAATTTTTTAAATAAATAGATGAGTGTGGTGTCTCATGCTGTATCCCAACACTT 3322
Db 26435 TTTTAAATAAATGGTGACAGTGGCTGAGTGCAGTGGCTCATGCTGTAAATCCCAACACTT 26494

QY 3323 TGGGAAGCGGGTCCGGGAGGATAGCTTGAGTCCAGCAGTTCAGACCACTCAGGGCAACA 3382
Db 26495 TGGGAGGCTGAGGCGAGGGGATGTGTTGAGCCCATAGTTTGAGACCAGCTGGCCCAACA 26554

QY 3383 CAGCAAGACCCCATATCTAAAAAACAACAAACAAATTAACCTGGGTATGGTTGTGC 3442
Db 26555 GGGTAAATCCCATCTCAACAAATAACACACACAAAAATTAGCTGGGCATGGTGTGT 26614

QY 3443 TCACCTGTAGTCCAAAGCTACAGGAAGCTGAGGAGGATCACTTACAGCCAGGAGG 3502
Db 26615 ACATCTGTGTCCAGCTACTCAGGAGGCCGAGGTGGGAGGATCACTCAGCCAGGAGG 26674
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; LENGTH: 156318
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)...(156318)
; OTHER INFORMATION: n = A,T,C or G, or insertion/deletion polymorphism (see Tables 1-
US-10-741-600-17574

Query Match          3.4%; Score 193; DB 22; Length 156318;
Best Local Similarity 70.8%; Pred. No. 4e-29;
Matches 271; Conservative 0; Mismatches 110; Indels 2; Gaps 1;

QY 3210 AAATCATGACATACGTTTAAATGATATTTTAAATACGTTAGCTATTAACCTTTTAAA 3269
Db 66635 ATATCTGTACAAACATCTGATTCACCTTTTCAAATCTTTAGTAGTAAAGTTAAATC 66576

QY 3270 TTTTAAATAAATAGATGAGTGTGGTGTCTATGCTGTAATCCCAACATTTGGGAAG 3329
Db 66575 TAAAGGTCAAAGATTGCTGGGTATGGTAGCTCAGGCTGTAAATTCCAACACTCTAGGAG 66516

QY 3330 CCGGTCGAGGAGTACGTGAGTCCAGCAGTTTGAGACCAGTCAGGGGCAACACAGAAG 3389
Db 66515 CCGAGCGGGCATATCGCTTGAGCCCGAGGGGTTTGAGACCAGTCCAGGCAACAGGCAAA 66456

QY 3390 ACCCCATATCTAAATAAACAACAAACAAACAAATTAACCTGGGTATGTTGTCTCACTG 3449
Db 66455 ACCCATCTCTACAAATAAATAACA--ATAATGAGCTGGGCATGTGGCAGCACCTG 66398

QY 3450 TAGTCAAGCTACACAGGAAGCTGAGGCAGAGGATCACTTGAGCCAGGAGGTTGAGGC 3509
Db 66397 TGGTCCAGCTACTTGGAGGCTGAGGCAGGAGGATGGCTTGAGCCAGGAGGTTGGGC 66338

QY 3510 TGCAGTGATCCATGAAGCGCTCTACACTCAGTCTGGGTGACAGTGCAAGAGCTGTCT 3569
Db 66337 TGCAGTGAGCTGAGCTGACTACTACTCAGTCTCCACCTAGGTGACAGAAATAGACCCCTGTCT 66278

QY 3570 CAAAAATAAATAAATAAATAA 3592
Db 66277 CAAAAATAAATAAATAAATAA 66255

RESULT 7
US-09-925-065A-552294
; Sequence 552294, Application US/09925065A
; Publication No. US20050228172A9
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single
; FILE OF INVENTION: Nucleotide Polymorphisms in the Human Genome
; FILE REFERENCE: 108827.135
; CURRENT APPLICATION NUMBER: US/09/925,065A
; CURRENT FILING DATE: 2001-08-08
; PRIOR APPLICATION NUMBER: US 60/243,096
; PRIOR FILING DATE: 2000-10-24
; PRIOR APPLICATION NUMBER: US 60/252,147
; PRIOR FILING DATE: 2000-11-20
; PRIOR APPLICATION NUMBER: US 60/250,092
; PRIOR FILING DATE: 2000-11-30
; PRIOR APPLICATION NUMBER: US 60/261,766
; PRIOR FILING DATE: 2001-01-16
; PRIOR APPLICATION NUMBER: US 60/289,846
; PRIOR FILING DATE: 2001-05-09
; NUMBER OF SEQ ID NOS: 957086
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 552294
; LENGTH: 536
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-925-065A-552294

Query Match          3.4%; Score 192.2; DB 13; Length 536;
Best Local Similarity 70.6%; Pred. No. 3.4e-30;
Matches 269; Conservative 1; Mismatches 109; Indels 2; Gaps 1;

QY 3212 ATCATGACATACGTTTAAATGATATTTTAAATACGTTAGGCTATAAACCTTTTAAAT 3271
Db 1 ATCTGTACAAACATCTGATTTTCACTTTTCAAAATCTTTTAGGTAGTAAAGTTAAATCTTA 60

QY 3272 TTTTAAATAAATAGATGAGTGTGGTGTCTATGCTGTAAATCCCAACACTTTGGGAAGCC 3331
Db 61 AAGGTCAAAGATTGCTGGGTATGGTAGCTCAGCCTGTAAATCCCAACACTCTAGGAGGCC 120

QY 3332 GGGTGGGAGGATAGCTTGGTCCAGCAGTTTGAGACCAGTCAAGGCAACACAGCAAGAC 3391
Db 121 GAGGGGGGRTATCGCTTGAGCCAGGGGTTTGAGACCAGTCAAGGCAACAGGCAAAAC 180

QY 3392 CCCATATCTAAATAAACAACAAACAAACAAATTAACCTGGGTATGGTGTGCTCACCTGTA 3451
Db 181 CCATCTCTACAAATAAATAAATAACA--ATAATGAGCTGGGCATGTGGCAGCAGCCTGTG 238

QY 3452 GTCCAAGCTACACAGGAAGCTGAGGCAGAAAGATCACTTTGAGCCCAAGGAGTTTGAGGCTG 3511
Db 239 GTCCAGCTACTTGGGAGGCTGAGGCAGGAGGATGGCTTGAGCCCAAGGATGTGGGCTG 298

QY 3512 CAGTGATCATGAACCGCTGCTACACTCAGTCTGGGTGACAGTGCAGAAAGCTGTCTCA 3571
Db 299 CAGTGAGCTGTGACTGTACTACTGCACTCCACTAGTGTGACAGAAATAAGACCTGTCTCA 358

QY 3572 AAAAAATAAATAAATAAATAA 3592
Db 359 AAAAAATAAATAAATAAATAA 379

RESULT 8
US-10-723-860-2320
; Sequence 2320, Application US/10723860
; Publication No. US20040253606A1
; GENERAL INFORMATION:
; APPLICANT: Aziz, Natasha
; APPLICANT: Ginsburg, Wendy M.
; APPLICANT: Zlotnik, Albert
; TITLE OF INVENTION: Methods of Diagnosis of Soft Tissue Sarcoma, Compositions &
; FILE OF INVENTION: Methods for Screening for Soft Tissue Sarcoma Modulators
; FILE REFERENCE: 05882.0193.NPUS01
; CURRENT APPLICATION NUMBER: US/10/723,860
; CURRENT FILING DATE: 2003-11-26
; PRIOR APPLICATION NUMBER: 60/429,739
; PRIOR FILING DATE: 2002-11-26
; NUMBER OF SEQ ID NOS: 8393
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 2320
; LENGTH: 135005
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-723-860-2320

Query Match          3.3%; Score 188.4; DB 21; Length 135005;
Best Local Similarity 71.8%; Pred. No. 3.5e-28;
Matches 260; Conservative 0; Mismatches 101; Indels 1; Gaps 1;

QY 3263 TTTTAAATTTTTTAAATAAATAGATGAGTGTGGTGTCTCATGCTGTATCCCAACACTT 3322
Db 26435 TTTTAAATAAATGGTGACAGTGGCTGAGTGCAGTGGCTCATGCTGTAAATCCCAACACTT 26494

QY 3323 TGGGAAGCGGGTCCGGGAGGATAGCTTGAGTCCAGCAGTTCAGACCACTCAGGGCAACA 3382
Db 26495 TGGGAGGCTGAGGCGAGGGGATGTGTTGAGCCCATAGTTTGAGACCAGCTGGCCCAACA 26554

QY 3383 CAGCAAGACCCCATATCTAAAAAACAACAAACAAATTAACCTGGGTATGGTTGTGC 3442
Db 26555 GGGTAAATCCCATCTCAACAAATAACACACACAAAAATTAGCTGGGCATGGTGTGT 26614

QY 3443 TCACCTGTAGTCCAAAGCTACAGGAAGCTGAGGAGGATCACTTACAGCCAGGAGG 3502
Db 26615 ACATCTGTGTCCAGCTACTCAGGAGGCCGAGGTGGGAGGATCACTCAGCCAGGAGG 26674
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[illegible]

RESULT 9
 US-10-756-149-1719
 ; Sequence 1719, Application US/10756149
 ; Publication No. US20050181375A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Aziz, Natasha
 ; APPLICANT: Zlotnik, Albert
 ; TITLE OF INVENTION: NOVEL METHODS OF DIAGNOSIS OF METASTATIC CANCER, COMPOSITIONS AND
 ; TITLE OF INVENTION: METHODS OF SCREENING FOR MODULATORS OF METASTATIC CANCER
 ; FILE REFERENCE: file
 ; CURRENT APPLICATION NUMBER: US/10/756,149
 ; CURRENT FILING DATE: 2004-01-12
 ; NUMBER OF SEQ ID NOS: 5818
 ; SOFTWARE: PatentIn version 3.2
 ; SEQ ID NO 1719
 ; LENGTH: 135005
 ; TYPE: DNA
 ; ORGANISM: Homo Sapiens
 US-10-756-149-1719

RESULT 10
US-10-380-124-10
; Sequence 10, Application US/10380124
; Publication No. US20040053874A1
; GENERAL INFORMATION:
; APPLICANT: Isis Pharmaceuticals, Inc.

```

; APPLICANT: Brett P. Monia
; APPLICANT: Susan M. Freier
; TITLE OF INVENTION: ANTISENSE MODULATION OF CLUSTERIN EXPRESSION
; FILE REFERENCE: RTS-0156
; CURRENT APPLICATION NUMBER: US/10/380,124
; CURRENT FILING DATE: 2003-03-10
; NUMBER OF SEQ ID NOS: 90
; SEQ ID NO 10
; LENGTH: 8133
; TYPE: DNA
; ORGANISM: Homo sapiens
; US-10-380-124-10

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RESULT 11
US-09-925-065A-123687/c
; Sequence 123687, Application US/09925065A
; Publication No. US20050228172A9
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single
; Nucleotide Polymorphisms in the Human Genome
; FILE REFERENCE: 108827.135
; CURRENT APPLICATION NUMBER: US/09/925,065A
; CURRENT FILING DATE: 2001-08-08
; PRIOR APPLICATION NUMBER: US 60/243,096
; PRIOR FILING DATE: 2000-10-24
; PRIOR APPLICATION NUMBER: US 60/252,147
; PRIOR FILING DATE: 2000-11-20
; PRIOR APPLICATION NUMBER: US 60/250,092
; PRIOR FILING DATE: 2000-11-30
; PRIOR APPLICATION NUMBER: US 60/361,766
; PRIOR FILING DATE: 2001-01-16
; PRIOR APPLICATION NUMBER: US 60/289,846
; PRIOR FILING DATE: 2001-05-09
; NUMBER OF SEQ ID NOS: 957086
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 123687
; LENGTH: 587
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-925-065A-123687

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Query Match 3.3%; Score 186; DB 13; Length 587;
Best Local Similarity 69.6%; Pred. No. 7.3e-29;

Query Match 3.3%; Score 186; DB 13; Length 587;
Best Local Similarity 69.6%; Pred. No. 7.3e-29;

Matches 281; Conservative 1; Mismatches 116; Indels 6; Gaps 2;

QY 3195 AAATAACAACTATTGAAATCATGACATACGTTTAAATGATATATTAAATACGTTAGGC 3254
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 DB 546 AATTTAAAAAATATTACAAATCATACAAATAGATGTTGAGTTAAATTTCAATTCAGTTGAC 487
 |||||
 QY 3255 TATAAACCTTTTAAATTTTTTAAAAAAATAGAT- ---GAGTGTGGTGCTCATGCTCT 3309
 |||||
 DB 486 TTTTWTGATTTGGTATTTTTTAAAAAAAAGGTTGACCATGTGTGGTGCTCTGTGCTGT 427
 |||||
 QY 3310 AATCCCAACACTTTTGGGAAGCCGGTTCGGAGGATAGCTTTGAGTCCAGCAGTTTGGAGCC 3369
 |||||
 DB 426 AATCCAGCACCTTTGGAGAGCTGAGTTGGAAGGATAGCTTTGAGACCAGGAGTTTGGAGCC 367
 |||||
 QY 3370 AGTCAGGGCAACACAGCAAGACCCCATATCTAAAAAACAACAAACAAATTAACCTG 3429
 |||||
 DB 366 AGCCTGGGCAACATGCGAAGACCTCATCTCTACTAAAAATAAAAAATAAAAAATAGCTA 307
 |||||
 QY 3430 GGTATGTTGTGCTCACTGTAGTCCAAAGCTACACAGGAAGCTTGAGGCAAGGATCACT 3489
 |||||
 DB 306 GGCATAGCAGTGTGTTCTATATAGTCCAGCTACTCAGGAGGCACAGGTGGAGGATCGCT 247
 |||||
 QY 3490 TGAGCCCGAGGAGTTGAGGCTGCAGTGATCCATGAAACGGCTGCTACACT- CAGTCTGGG 3548
 |||||
 DB 246 TGAACCCAGGAGTTGAGGCTGCAGTGAGTGTGATCACACCACTGCCTCCAGCCTAGG 187
 |||||
 QY 3549 TGACAGTGCAGAAGCTGTCTCAAAATATATAATTAATAAATA 3592
 |||||
 DB 186 TGACAGAGAAGACCTTGTCTCAAGAAATTAAGCAAAACAAATAA 143
 |||||

RESULT 12
 US-09-984-429-513
 ; Sequence 513, Application US/09984429
 ; Publication No. US20040010132A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Rosen et al.
 ; TITLE OF INVENTION: 53 Human Secreted Proteins
 ; FILE REFERENCE: P2018P2
 ; CURRENT APPLICATION NUMBER: US/09/984,429
 ; CURRENT FILING DATE: 2001-10-30
 ; PRIOR APPLICATION NUMBER: 60/244,591
 ; PRIOR FILING DATE: 2000-11-01
 ; PRIOR APPLICATION NUMBER: 09/288,143
 ; PRIOR FILING DATE: 1999-04-08
 ; PRIOR APPLICATION NUMBER: PCT/US98/21142
 ; PRIOR FILING DATE: 1998-10-08
 ; PRIOR APPLICATION NUMBER: 60/061,463
 ; PRIOR FILING DATE: 1997-10-09
 ; PRIOR APPLICATION NUMBER: 60/061,529
 ; PRIOR FILING DATE: 1997-10-09
 ; PRIOR APPLICATION NUMBER: 60/071,498
 ; PRIOR FILING DATE: 1997-10-09
 ; PRIOR APPLICATION NUMBER: 60/061,527
 ; PRIOR FILING DATE: 1997-10-09
 ; PRIOR APPLICATION NUMBER: 60/061,536
 ; PRIOR FILING DATE: 1997-10-09
 ; PRIOR APPLICATION NUMBER: 60/061,532
 ; PRIOR FILING DATE: 1997-10-09
 ; NUMBER OF SEQ ID NOS: 727
 ; SOFTWARE: PatentIn Ver. 2.0
 ; SEQ ID NO 513
 ; LENGTH: 18861
 ; TYPE: DNA
 ; ORGANISM: Homo sapiens
 US-09-984-429-513

Query Match 3.3%; Score 186; DB 11; Length 18861;
 Best Local Similarity 76.1%; Pred. No. 4.2e-28;
 Matches 242; Conservative 0; Mismatches 75; Indels 1; Gaps 1;

QY 3265 TTAATATTTTAAAAAATAGATGATGTGGTGCTCATGCTGTAAATCCCAACTTTG 3324
 |||||

Db 158 CTTGAGCCTGGAGGTCAGGCTGCAAGTGTGAGCGGAGATTGCACCACCTGCACCTCCAGCCTG 99
Qy 3547 GGTGACAGTCAAGAGCTGCTCTCAAAAATAATAATAATAATAATAATAATACTTTTAAAAAA 3606
Db 98 GGCTACAGAACCAAGTCTCTCTCAAAAATAATAATAATAATAATAATAATAAGGAAGAAAGACAATA 39
Qy 3607 CAAAAATTAATTAATTTTA 3626
Db 38 TAGATATGTTCCCTTTCTA 19

RESULT 14
US-09-925-065A-907871/c
; Sequence 907871, Application US/09925065A
; Publication No. US20050228172A9
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single
; FILE REFERENCE: 108827.135
; CURRENT APPLICATION NUMBER: US/09/925,065A
; PRIOR FILING DATE: 2001-08-08
; PRIOR APPLICATION NUMBER: US 60/243,096
; PRIOR FILING DATE: 2000-10-24
; PRIOR APPLICATION NUMBER: US 60/252,147
; PRIOR FILING DATE: 2000-11-20
; PRIOR APPLICATION NUMBER: US 60/250,092
; PRIOR FILING DATE: 2000-11-30
; PRIOR APPLICATION NUMBER: US 60/261,766
; PRIOR FILING DATE: 2001-01-16
; PRIOR APPLICATION NUMBER: US 60/289,846
; PRIOR FILING DATE: 2001-05-09
; NUMBER OF SEQ ID NOS: 957086
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 907871
; LENGTH: 610
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-925-065A-907871

Query Match 3.3%; Score 185.6; DB 13; Length 610;
Best Local Similarity 71.6%; Pred. No. 9.1e-29;
Matches 272; Conservative 0; Mismatches 104; Indels 4; Gaps 2;
Qy 3251 AGGCTATAAACCTTTTAAATTTTAAAAAATAGATGAGTGTGGTGGCTCATGCCCTGTA 3310
Db 402 AGGTTTTCATGTTTAAAAAAGAAAACAAGGGGCTGACATGGTGGCTCATGCCCTGTA 343
Qy 3311 ATCCCAACACTTTGGGAAGCGGGTCGGGAGGATAGCTTGGTCCAGCAGTTTGGAGACCA 3370
Db 342 ATCCAGCACTTTGGGAGGCAAGGCAAGTGTGTTGCTTGGAGCCAGGAGTTTGGAGACCA 283
Qy 3371 GTGAGGCAACAGCAGCAGCAGCCATATCT---AAAAAACAACAACAACAATAATACC 3427
Db 282 GCCTGAACAACATAGGAGAGCTGTGCTCTACAAAAAATAAAAAAATAAAAAATGGC 223
Qy 3428 TGGGTATGTTGTGCTCACCTGTAGTCCAGGCTACACAGGAAGCTGAGGAGGAGGATCA 3487
Db 222 TGGGGTGTGGTGGAGCCTGTAGTCCAGCCTACTTCCAGGAGCTGAGGAGGAGGATCA 163
Qy 3488 CTTGAGCCCAAGGAGTTGAGGCTGCAGTATCCATGAACCGCGTGTCTACT-CAGTCTG 3546
Db 162 CTTGAGCCTGGAGGTCAGGCTGCAGTGCAGCCAGATTGCACCACTGCACCTCCAGCCTG 103
Qy 3547 GGTGACAGTCAAGAGCTGCTCTCAAAAATAATAATAATAATAATAATACTTTTAAAAAA 3606
Db 102 GGCTACAGAACCAAGTCTCTCTCAAAAATAATAATAATAATAATAATAAGGAAGAAAGACAATA 43
Qy 3607 CAAAAATTAATTAATTTTA 3626
Db 42 TAGATATGTTCCCTTTCTA 23

RESULT 15
US-10-027-632-181221/c
; Sequence 181221, Application US/10027632
; Publication No. US20020198371A1
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
; FILE REFERENCE: 108827.129
; CURRENT APPLICATION NUMBER: US/10/027,632
; PRIOR FILING DATE: 2002-04-30
; PRIOR APPLICATION NUMBER: US 60/218,006
; PRIOR FILING DATE: 2000-07-12
; PRIOR APPLICATION NUMBER: US 60/198,676
; PRIOR FILING DATE: 2000-04-20
; PRIOR APPLICATION NUMBER: US 60/193,483
; PRIOR FILING DATE: 2000-03-29
; PRIOR APPLICATION NUMBER: US 60/185,218
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: US 60/167,363
; PRIOR FILING DATE: 1999-11-23
; PRIOR APPLICATION NUMBER: US 60/156,358
; PRIOR FILING DATE: 1999-09-28
; PRIOR APPLICATION NUMBER: US 60/146,002
; PRIOR FILING DATE: 1999-08-09
; NUMBER OF SEQ ID NOS: 325720
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 181221
; LENGTH: 611
; TYPE: DNA
; ORGANISM: Human
US-10-027-632-181221

Query Match 3.3%; Score 185.6; DB 14; Length 611;
Best Local Similarity 71.6%; Pred. No. 9.1e-29;
Matches 272; Conservative 0; Mismatches 104; Indels 4; Gaps 2;
Qy 3251 AGGCTATAAACCTTTTAAATTTTAAAAAATAGATGAGTGTGGTGGCTCATGCCCTGTA 3310
Db 410 AGGTTTTCATGTTTAAAAAAGAAAACAAGGGGCTGAGCATGGTGGCTCATGCCCTGTA 351
Qy 3311 ATCCCAACACTTTGGGAAGCGGGTCGGGAGGATAGCTTGGTCCAGCAGTTTGGAGACCA 3370
Db 350 ATCCAGCACTTTGGGAGGCAAGGCAAGTGTGTTGCTTGGAGCCAGGAGTTTGGAGACCA 291
Qy 3371 GTGAGGCAACAGCAGCAGCAGCCATATCT---AAAAAACAACAACAACAATAATACC 3427
Db 290 GCCTGAACAACATAGGAGAGCTGTGCTCTACAAAAAATAAAAAAATAAAAAATGGC 231
Qy 3428 TGGGTATGTTGTGCTCACCTGTAGTCCAGGCTACACAGGAAGCTGAGGAGGAGGATCA 3487
Db 230 TGGGGTGTGGTGGAGCCTGTAGTCCAGCCTACTTCCAGGAGCTGAGGAGGAGGATCA 171
Qy 3488 CTTGAGCCCAAGGAGTTGAGGCTGCAGTATCCATGAACCGCGTGTCTACT-CAGTCTG 3546
Db 170 CTTGAGCCTGGAGGTCAGGCTGCAGTGCAGCCAGATTGCACCACTGCACCTCCAGCCTG 111
Qy 3547 GGTGACAGTCAAGAGCTGCTCTCAAAAATAATAATAATAATAATAATACTTTTAAAAAA 3606
Db 110 GGCTACAGAACCAAGTCTCTCTCAAAAATAATAATAATAATAATAATAAGGAAGAAAGACAATA 51
Qy 3607 CAAAAATTAATTAATTTTA 3626
Db 50 TAGATATGTTCCCTTTCTA 31

Search completed: November 2, 2005, 04:52:20
Job time : 4073 secs

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